SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			17.27 4.462e-11 47-70 PR00449D 10.79 7.120e-11 109-123
235	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e-10 251-265 PR00019B 11.36 5.320e-09 119-133 PR00019B 11.36 1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e-10 245-259 PR00019B 11.36 5.320e-09 113-127 PR00019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 8.448e-09 67-81
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e-10 616-635
241	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e-10 616-635
244	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e-12 54-64
245	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e-09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e-40 186-239 BL00246B 20.32 1.000e-40 305-351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e-24 70-90 BL00246C 15.56 4.857e-22 150-175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e-10 253-275
254	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.000e-09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 6.045e-09 61-88
256	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e-10 421-435
258	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e-08 87-104 PR00094D 12.52 2.731e-14 161-177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e-13 39-54 PR00094E 11.25 7.333e-13 178-193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e-13 60-91
262	BL00388	Proteasome A-type subunits proteins.	BL00388A 23.14 1.000e-40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e-21 153-184 BL00388C 18.79 8.147e-16 126-148
264	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 5.821e-09 91-101
267	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.529e-09 241-257
270	BL00226	Intermediate filaments proteins.	BL00226D 19.10 1.000e-37 362-409 BL00226B

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			23.86 8.043e-35 196-244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e-15 96-111
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	PD02952C 15.76 9.731e-16 235-265 PD02952B 15.57 5.625e-09 215-229
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e-40 106-160 PD02929B 18.36 8.800e-17 179-199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e-09 213-250
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e-11 39-59
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e-13 137-184 BL00052B 15.17 5.143e-12 208-235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e-13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e-21 51-68 PR00319B 11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e-23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e-21 38-55 PR00319B 11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366e-09 149-163
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e-12 203-216
295	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e-15 322-339 BL00028 16.07 9.471e-14 433-450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e-13 760-777 BL00028 16.07 9.550e-13 788-805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e-12 461-478 BL00028 16.07 8.435e-12 844-861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e-11 211-228 BL00028 16.07 5.154e-11 732-749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e-11 816-833 BL00028 16.07 7.231e-11 676-693 BL00028 16.07 9.654e-11 564-581

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			BL00028 16.07 4.086e-09 517-534 BL00028 16.07 7.429e-09 489-506
296	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.333e-16 111-136 BL00215A 15.82 2.723e-11 10-35 BL00215B 10.44 9.526e-11 152-165 BL00215B 10.44 7.375e-10 59-72 BL00215A 15.82 9.824e-10 205-230
302	PF00953	Glycosyl transferase.	PF00953C 19.70 8.773e-34 236-269 PF00953A 19.68 5.000e-25 102-129 PF00953B 6.17 1.000e-13 182-194
304	PF00152	tRNA synthetases class II.	PF00152D 21.30 8.364e-28 422-461 PF00152C 28.03 9.250e-21 220-257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e-11 44-67
305	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.250e-35 37-76
306	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 5.840e-09 92-135
307	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-09 1167-1186
308	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 5.091e-13 188-212 PR00237G 19.63 7.207e-13 268-295 PR00237A 11.48 4.375e-11 24-49 PR00237C 15.69 3.057e-10 101-124 PR00237D 8.94 4.750e-10 137-159 PR00237F 13.57 5.364e-10 230-255 PR00237B 13.50 9.438e-10 57-79
309	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 7.577e-24 315-339 BL00522F 14.90 1.310e-15 470-494 BL00522A 25.52 1.265e-14 179-226 BL00522E 19.63 8.615e-14 430-460 BL00522B 27.30 9.625e-12 267-313
310	BL00326	Tropomyosins proteins.	BL00326D 8.76 5.235e-10 856-897
312	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.706e-14 151-174 BL00290B 13.17 9.000e-12 211-229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-40 34-85 BL00345A 13.96 9.217e-16 1-20
315	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 5.091e-15 63-76
317	BL01020	SAR1 family proteins.	BL01020C 15.35 3.198e-17 79-130
318	BL00216	Sugar transport proteins.	BL00216B 27.64 4.696e-11 164-214
320	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109B 12.27 4.814e-10 216-235

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		SIGNATURE	
321	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.688e-10 329-372
322	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 8.765e-12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e-30 183-236 BL01241 35.81 3.222e-13 282-335
326	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e-12 515-566 BL00412D 16.54 5.705e-11 516-567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e-09 514-565 BL00412D 16.54 1.918e-09 513-564 BL00412D 16.54 2.102e-09 520-571
328	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e-20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e-18 370-418 BL00232B 32.79 5.500e-16 258-306 BL00232B 32.79 9.384e-15 475-523 BL00232C 10.65 2.537e-12 256-274 BL00232C 10.65 4.326e-11 368-386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e-11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e-18 27-49
333	BL01016	Glycoprotease family proteins.	BL01016C 22.84 3.925e-32 70-115 BL01016E 14.88 5.286e-19 149-177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e-11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e-10 4-19 BL01016F 13.34 1.563e-09 200-212 BL01016B 8.93 8.855e-09 38-50
339	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.500e-11 17-61
340	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 1.231e-33 10-49
341	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e-09 55-109
342	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.400e-30 16-55
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-40 20-68
346	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.764e-11 135-154
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

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		CATALYTIC DOMAIN SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.783e-13 100-116 BL01187B 12.04 8.435e-13 276-292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e-10 54-70 BL01187B 12.04 5.725e-09 231-247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e-11 542-553
355	PF00628	PHD-finger.	PF00628 15.84 1.000e-11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e-09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e-15 261-274 PD00066 13.92 6.500e-13 233-246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e-13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e-09 71-126 PF00791B 28.49 7.440e-09 184-239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e-11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e-10 73-95 PR00450C 12.22 3.278e-09 109-131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e-09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e-09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e-09 1038-1092
367	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e-09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e-09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 9.000e-15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e-14 30-49 PR00011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e-09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e-12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.757e-34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170R 6.48 2.739e-

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			10 88-118
380	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 1.000e-23 276-307 BL00107B 13.31 1.692e-12 342-358
381	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 5.714e-12 50-66
382	PR00624	HISTONE H5 SIGNATURE	PR00624G 4.08 4.900e-09 524-544
384	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181
385	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-09 67-80
386	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 6.000e-10 97-130
388	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e-13 516-529
389	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.667e-09 151-174
390	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.200e-15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e-11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e-09 272-285 BL00215B 10.44 8.500e-09 165-178
394	BL00674	AAA-protein family proteins.	BL00674B 4.46 2.723e-16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.579e-11 141-155
398	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761B 9.93 6.764e-09 55-74
399	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.907e-10 118-142
401	PF00676	Dehydrogenase E1 component.	PF00676B 24.71 8.071e-18 331-369 PF00676D 14.40 3.854e-15 486-506 PF00676C 16.88 9.182e-14 454-478
402	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 4.673e-28 4432-4469 BL00514G 15.98 6.092e-14 4555-4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e-10 4519-4534 BL00514H 14.95 4.955e-10 4584-4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e-09 105-140
404	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.450e-10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e-09 50-64 PR00019B 11.36 1.000e-09 96-110
405	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e-20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e-18 358-406 BL00232B 32.79 5.500e-16 246-

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			294 BL00232B 32.79 9.384e-15 463-511 BL00232C 10.65 2.537e-12 244-262 BL00232C 10.65 4.326e-11 356-374 BL00232C 10.65 7.261e-11 461-479 BL00232C 10.65 7.457e-11 27-45
407	PF00426	Outer Capsid protein VP4 (Hemagglutinin).	PF00426S 15.67 5.634e-09 902-940
409	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.695e-09 126-180
410	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 2.731e-09 252-275
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e-09 86-100
412	BL00603	Thymidine kinase cellular-type proteins.	BL00603B 11.39 8.500e-09 542-557
415	BL00866	Carbamoyl-phosphate synthase subdomain proteins.	BL00866B 36.29 3.571e-31 245-291 BL00866C 23.26 9.000e-25 331-366
418	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 6.114e-09 590-602
421	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.955e-14 23-78 PF00791B 28.49 3.653e-12 273-328 PF00791B 28.49 4.273e-11 156-211 PF00791B 28.49 7.818e-11 89-144 PF00791B 28.49 1.524e-10 56-111 PF00791C 20.98 3.559e-09 37-76 PF00791C 20.98 5.235e-09 170-209 PF00791C 20.98 5.235e-09 381-420 PF00791B 28.49 6.202e-09 189-244 PF00791B 28.49 7.028e-09 435-490 PF00791B 28.49 8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e-28 1645-1679
425	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 5.881e-10 228-251
429	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.600e-11 31-40
431	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 1.844e-34 490-536 BL00039A 18.44 5.615e-19 205-244 BL00039B 19.19 8.920e-16 251-277 BL00039C 15.63 5.781e-15 333-357
432	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 7.652e-12 169-185
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e-10 382-405
436	BL00415	Synapsins proteins.	BL00415N 4.29 8.643e-11 195-239 BL00415N 4.29 3.036e-09 809-853
443	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE	PR00834F 10.91 6.040e-11 221-234
446	PF01140	Matrix protein (MA),	PF01140D 15.54 9.663e-

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		p15.	10 183-218 PF01140D 15.54 3.093e-09 246-281
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PR00568G 13.95 5.551e-09 39-53
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e-10 47-59
452	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e-09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e-25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e-17 230-249 PR00380B 12.64 4.724e-16 194-212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e-24 246-267 PR00253B 13.47 2.000e-23 272-294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e-21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e-09 910-937
471	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.200e-12 33-44
472	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.721e-09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e-12 814-852
474	BL00481	Thiol-activated cytolysins proteins.	BL00481E 13.07 8.909e-09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e-09 393-408
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 1.900e-38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e-19 451-473 PR00405B 11.83 4.333e-18 430-448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e-10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e-09 937-952 PR00049D 0.00 8.322e-09 939-954
486	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e-23 653-673 PR00007A 19.33 6.192e-22 626-653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e-13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e-09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e-12 3-21
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.882e-27 30-69 PD01066 19.43 3.430e-10 71-110
490	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.864e-09 663-678
492	BL01128	Shikimate kinase proteins.	BL01128A 18.84 6.464e-17 58-92
497	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

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		polyprotein).	15 21-71
498	BL00120	Lipases, serine proteins.	BL00120B 11.37 7.923e-09 185-200
500	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.353e-11 299-318
501	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 8.579e-12 131-146
505	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e-17 492-510
508	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 5.800e-19 705-722
509	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417E 20.62 2.938e-16 362-395 DM01417D 11.08 3.800e-13 322-338
510	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-09 346-370
511	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-09 293-317
512	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-09 366-390
513	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e-40 110-160 PD01841B 14.35 1.000e-40 181-222 PD01841D 17.87 1.000e-40 243-295 PD01841F 13.36 1.000e-40 333-382 PD01841G 24.26 1.000e-40 386-440 PD01841L 18.42 1.000e-40 968-1010 PD01841I 23.00 4.545e-37 762-804 PD01841E 18.60 3.750e-36 295-333 PD01841J 14.94 6.023e-35 851-888 PD01841H 21.30 2.909e-33 490-527 PD01841K 14.81 7.088e-33 924-954 PD01841C 13.78 9.386e-23 222-243 PD01841M 10.82 8.594e-21 1054-1073 PD01841I 23.00 2.667e-13 549-591
514	PR00153	CYCLOPHILIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153C 11.01 7.188e-13 95-111 PR00153E 9.10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 23.87 7.188e-12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-12 1018-1052
517	BL00242	Integrins alpha chain proteins.	BL00242C 16.86 8.320e-09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-39 20-68 DM00031B 15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 8.375e-10 61-95
526	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 3.308e-12 322-343 PF00789C 20.98 5.269e-09 367-392
528	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 1.500e-16 120-164

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529	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 3.893e-09 60-73
532	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 123-148
533	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 97-122
534	BL00098	Thiolases acyl-enzyme intermediate proteins.	BL00098C 21.65 2.800e-38 181-227 BL00098B 32.59 5.345e-38 86-141 BL00098D 26.30 8.364e-35 245-288 BL00098E 22.12 1.000e-34 314-352 BL00098F 10.18 4.971e-22 365-386 BL00098A 10.60 6.455e-11 38-50
535	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370E 11.96 7.429e-22 321-340 PR00370D 16.33 6.143e-21 185-204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e-21 27-46 PR00370C 12.72 3.500e-20 140-157 PR00370A 3.35 6.442e-17 4-20
536	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.429e-16 285-302 BL00028 16.07 6.294e-14 341-358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e-11 397-414 BL00028 16.07 4.462e-11 453-470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e-10 313-330
537	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-15 844-881
538	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-15 819-856
539	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE SIGNATURE	PR00985A 12.10 9.000e-10 357-375
541	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 1.000e-40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e-30 179-218 PD02102C 26.34 8.929e-26 100-146
543	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-10 48-65 BL00028 16.07 6.400e-10 193-210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e-09 78-95
545	BL00250	TGF-beta family proteins.	BL00250A 21.24 8.000e-31 293-329 BL00250B 27.37 5.286e-24 354-390
547	PR00319	BETA G-PROTEIN	PR00319B 11.47 2.714e-

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		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210-227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	BL01204A 17.74 1.000e-40 8-56 BL01204D 16.42 1.000e-40 177-221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e-22 141-160 BL01204B 15.41 4.333e-16 102-116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.364e-15 255-276
551	PF00632	HECT-domain (ubiquitin-transferase).	PF00632C 20.66 3.302e-23 1569-1601 PF00632B 18.45 3.700e-21 1515-1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e-14 187-205 BL00290A 20.89 2.059e-14 130-153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e-09 846-879
559	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e-09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e-32 118-155
564	BL00141	Eukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e-10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e-15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.977e-13 229-268
569	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.000e-19 118-149 BL00107B 13.31 5.500e-15 183-199
570	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.000e-19 118-149 BL00107B 13.31 5.500e-15 183-199
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e-34 454-483 PR00193C 12.60 2.636e-31 223-251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e-22 115-135 PR00193E 19.47 6.559e-19 508-537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e-34 470-499 PR00193C 12.60 2.636e-31 239-267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e-22 115-135 PR00193E 19.47 6.559e-19 524-553
575	BL00752	XPA protein.	BL00752B 19.17 9.703e-10 885-929
576	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.000e-09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

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		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952-965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e-09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 9.000e-11 217-231 PR00019B 11.36 1.360e-09 386-400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e-09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e-25 275-296 PR00253B 13.47 7.923e-24 301-323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e-20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e-11 1233-1252 PR00343C 16.85 5.500e-11 333-352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e-10 1491-1510 PR00343C 16.85 8.230e-10 1686-1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e-37 79-126 DM01537B 21.63 9.491e-30 916-963 DM01537A 15.14 3.186e-11 784-804
586	PF00013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e-13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e-13 261-276 BL00478B 14.79 7.709e-09 321-336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e-15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e-15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e-12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e-16 558-576 PR00205A 14.73 9.308e-13 542-558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e-10 336-354
596	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.789e-18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e-10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e-27 985-1014 BL00242C 16.86 4.115e-26 286-316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e-12 189-199 BL00242D 13.57 3.455e-11 421-446 BL00242A 13.80

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			5.000e-11 61-73 BL00242D 13.57 4.986e-10 291-316
601	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 5.610e-09 198-213
602	PR00278	PANCREATIC HORMONE SIGNATURE	PR00278A 12.43 4.569e-10 331-348
603	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 3.250e-12 170-183
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e-09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e-10 295-339
606	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e-13 335-358
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-15 211-228
612	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.411e-10 877-897 DM01206B 10.69 8.027e-10 861-881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10:69 1.456e-09 859-879 DM01206B 10.69 1.797e-09 879-899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e-09 898-918 DM01206B 10.69 7.949e-09 871-891 DM01206B 10.69 8.291e-09 767-787
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 2.023e-28 129-158 PD02699C 24.84 1.000e-27 317-364 PD02699B 18.28 1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455
617	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 5.143e-12 531-551 DM01206B 10.69 2.603e-10 535-555
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e-21 561-582
622	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e-10 647-692 BL00239C 18.75 8.304e-10 543-566
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407K 9.94 8.448e-09 326-339
624	BL00641	Respiratory-chain NADH dehydrogenase 75 Kd	BL00641C 21.10 1.000e-40 157-202 BL00641E

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		subunit proteins.	24.37 1.000e-40 255-308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e-37 48-80 BL00641B 12.62 5.846e-34 113-139 BL00641D 13.23 9.308e-29 216-240
627	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	PR00103E 17.80 2.500e-18 367-380 PR00103B 13.39 2.080e-14 297-312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e-12 346-358 PR00103C 15.68 1.000e-11 334-344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e-10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 6.211e-16 4-22
631	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.500e-14 37-50
632	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e-10 1324-1344 DM01206B 10.69 4.822e-10 1276-1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e-10 1280-1300 DM01206B 10.69 4.532e-09 1320-1340 DM01206B 10.69 7.266e-09 1326-1346
635	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.600e-23 145-176 BL00107B 13.31 2.636e-13 211-227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e-30 101-143 BL00657B 22.27 7.750e-26 149-192
637	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-10 607-623
643	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
647	PF00628	PHD-finger.	PF00628 15.84 2.350e-13 385-400 PF00628 15.84 3.455e-12 464-479
648	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 4.000e-25 332-357 BL01129C 25.56 8.200e-23 236-279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 3.908e-10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e-13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e-12 1026-1045
653	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 4.000e-24 253-274 PR00253C 13.85 8.800e-24 313-335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

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			20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e-11 969-997 PD01719A 12.89 3.961e-10 128-156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e-09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354C 6.61 8.397e-09 563-578
658	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354C 6.61 8.397e-09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e-13 539-572 DM00215 19.43 4.750e-12 549-582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e-10 548-581 DM00215 19.43 4.054e-10 550-583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e-10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e-09 224-236
661	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e-23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-10 596-610
666	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.988e-10 704-720
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e-16 135-178
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e-09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e-09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 1.000e-34 356-410 PD00131C 19.59 1.346e-26 504-542
673	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667G 15.33 7.557e-10 106-123
674	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e-13 593-608 PR00320B 12.19 4.115e-12 635-650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e-10 635-650 PR00320C 13.01 6.400e-10 593-608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e-13 572-587 PR00320B 12.19 4.115e-12 614-

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			629 PR00320C 13.01 8.435e-11 696-711 PR00320C 13.01 2.800e-10 614-629 PR00320C 13.01 6.400e-10 572-587 PR00320B 12.19 3.250e-09 572-587
676	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.667e-09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 3.700e-16 225-236 PF00642 11.59 7.900e-12 187-198
680	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.754e-10 286-296
681	BL00019	Actinin-type actin-binding domain proteins.	BL00019D 15.33 4.200e-19 227-257
682	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 4.000e-09 99-118
687	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.500e-10 538-553
689	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.	BL01024A 10.26 1.000e-40 22-69 BL01024B 8.91 1.000e-40 86-127 BL01024C 7.80 1.000e-40 146-185 BL01024D 13.22 1.000e-40 185-222 BL01024E 11.96 1.000e-40 222-266 BL01024F 9.42 1.000e-40 266-317 BL01024G 11.09 1.000e-40 317-349 BL01024H 13.88 1.000e-40 389-442
691	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.071e-31 152-195
692	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e-09 45-57
693	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e-09 45-57
694	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e-09 58-70
696	BL00680	Methionine aminopeptidase subfamily 1 proteins.	BL00680 14.37 5.304e-17 173-195
697	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 3.418e-11 242-265
698	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930E 15.41 1.367e-37 170-215 DM01930F 14.16 8.232e-28 267-303 DM01930B 19.86 9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X SIGNATURE	PR00869A 12.80 1.281e-16 245-263
701	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.174e-10 77-91 PR00048A 10.52 6.870e-10 133-147 PR00048A 10.52 8.826e-10 105-119 PR00048A 10.52 5.320e-09 161-175
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e-25 326-356 BL00523A 13.36 5.050e-16 38-55 BL00523B 8.64 5.909e-15 86-98 BL00523C 12.64 5.500e-13 137-

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			148 BL00523D 9.89 1.844e-11 290-302 BL00523G 9.46 5.500e-10 513-523 BL00523F 10.85 6.351e-09 413-424
703	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e-12 376-390 PR00048B 6.02 1.000e-10 334-344 PR00048B 6.02 1.474e-09 364-374
707	PD00787	SYNTHASE BIOSYNTHESIS TRANSFERASE.	PD00787A 14.84 8.941e-14 66-82
708	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 8.500e-10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Y 10.69 4.977e-38 425-465 DM01354X 13.86 7.300e-34 376-415 DM01354V 12.97 4.923e-17 311-358 DM01354W 12.64 5.596e-10 356-376
713	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 7.545e-27 450-496 BL00039A 18.44 2.537e-18 147-186 BL00039C 15.63 2.216e-14 280-304 BL00039B 19.19 1.947e-13 194-220
715	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 4.981e-10 150-161
717	PF00777	Sialyltransferase family.	PF00777C 18.60 4.035e-21 106-161
718	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-39 20-68 DM00031B 15.41 2.688e-28 84-118 DM00031C 12.79 1.300e-12 131-142
719	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243B 17.54 1.000e-40 131-172 BL00243C 16.42 1.000e-40 172-208 BL00243D 24.07 1.000e-40 222-274 BL00243F 22.63 1.000e-40 314-358 BL00243I 31.77 6.571e-39 607-650 BL00243E 16.70 3.077e-35 274-304 . BL00243G 21.38 3.625e-34 358-400 BL00243H 17.53 5.235e-29 567-593 BL00243A 17.61 3.250e-21 63-84 BL00243H 17.53 7.167e-16 477-503 BL00243H 17.53 2.304e-11 524-550 BL00243H 17.53 5.304e-11 606-632 BL00243I 31.77 1.380e-09 610-653
720	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 8.022e-09 20-36
722	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704D 11.05 5.909e-34 135-161 PR00704F 13.61 7.000e-26 190-218 PR00704E 12.55 8.071e-26 165-189

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			PR00704B 17.94 2.241e-23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e-18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-09 169-187
727	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.125e-13 277-292 PR00320A 16.74 1.310e-11 277-292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e-11 323-338 PR00320B 12.19 4.343e-10 323-338 PR00320B 12.19 6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e-16 288-307 PR00195E 9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.082e-10 787-798
738	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039A 18.44 2.565e-28 26-65 BL00039D 21.67 2.105e-20 338-384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e-11 73-99
739	BL01289	TSC-22 / dip / bun family proteins.	BL01289A 12.18 8.909e-31 326-353 BL01289B 10.45 9.571e-17 353-383
742	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 7.078e-12 41-81
743	BL00965	Phosphomannose isomerase type I proteins.	BL00965C 23.78 1.000e-40 256-305 BL00965B 17.77 1.600e-25 126-153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e-25 231-273 BL00021B 13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain proteins.	BL00612B 11.35 2.034e-11 93-126
749	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.880e-10 135-157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e-11 384-429 BL00795C 17.06 9.444e-11 370-415
754	BL00051	Ribosomal protein L39e proteins.	BL00051 20.92 1.935e-16 4-50
755	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e-09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e-12 99-150
762	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e-40 33-88
763	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 9.137e-10 206-240
764	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.800e-29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e-10 309-324 BL01208B 15.83 8.031e-10 165-

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			180 BL01208B 15.83 4.162e-09 85-100
770	BL00031	Nuclear hormones receptors DNA-binding region proteins.	BL00031A 19.55 9.571e-32 208-241 BL00031B 22.25 5.500e-27 242-274
772	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.450e-18 4-26 PR00449E 13.50 3.520e-14 142-165 PR00449C 17.27 3.032e-13 44-67 PR00449D 10.79 8.579e-13 107-121 PR00449B 14.34 3.455e-11 27-44
773	BL00523	Sulfatases proteins.	BL00523E 19.27 9.333e-23 299-329 BL00523A 13.36 2.200e-13 47-64 BL00523B 8.64 2.607e-13 91-103 BL00523D 9.89 7.923e-12 224-236 BL00523C 12.64 4.512e-10 141-152 BL00523F 10.85 5.821e-10 373-384
775	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 568-585
776	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 621-638
777	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 595-612
778	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 8.412e-11 322-341 BL00030A 14.39 7.000e-10 220-239
779	PR00079	GLUCOSE-6-PHOSPHATE DEHYDROGENASE SIGNATURE	PR00079B 12.98 2.929e-26 193-222 PR00079E 16.65 4.150e-23 348-375 PR00079C 8.68 6.351e-16 246-264 PR00079D 13.51 7.070e-16 264-281 PR00079A 16.12 6.769e-13 169-183
781	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.250e-17 10-35 BL00215A 15.82 6.000e-16 221-246 BL00215A 15.82 7.857e-12 108-133 BL00215B 10.44 9.526e-11 168-181
783	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 6.276e-09 159-173
785	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.	BL00690B 13.38 1.000e-12 147-165 BL00690A 6.87 5.320e-10 114-124 BL00690C 7.51 3.189e-09 218-228
786	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 8.500e-16 50-73 PR00449A 13.20 5.235e-14 8-30 PR00449E 13.50 2.853e-11 150-173 PR00449D 10.79 1.545e-09 111-125
788	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 8.767e-10 1-21
790	BL00915	Phosphatidylinositol 3- and 4-kinases proteins.	BL00915C 22.43 9.182e-39 725-764 BL00915B

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			22.78 5.050e-33 633-671 BL00915D 27.02 1.529e-21 795-831 BL00915A 10.09 1.000e-13 395-407
791	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 6.294e-10 120-138 PR00208A 12.59 6.294e-10 121-139 PR00208A 12.59 6.294e-10 122-140 PR00208A 12.59 6.294e-10 123-141 PR00208A 12.59 6.294e-10 124-142 PR00208A 12.59 6.294e-10 125-143 PR00208A 12.59 6.294e-10 126-144 PR00208A 12.59 6.294e-10 127-145 PR00208A 12.59 6.294e-10 128-146 PR00208A 12.59 6.294e-10 129-147 PR00208A 12.59 7.411e-09 130-148 PR00208A 12.59 7.658e-09 131-149 PR00208A 12.59 7.904e-09 132-150 PR00208A 12.59 8.274e-09 118-136 PR00208A 12.59 8.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e-16 302-320 PR00205A 14.73 1.257e-11 284-300 PR00205C 13.65 1.333e-11 337-352
796	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e-12 196-247 BL00412D 16.54 5.705e-11 197-248 BL00412D 16.54 7.848e-10 199-250 BL00412D 16.54 1.827e-09 195-246 BL00412D 16.54 1.918e-09 194-245 BL00412D 16.54 2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.339e-13 40-58
799	BL01052	Calponin family repeat proteins.	BL01052C 18.51 1.000e-40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e-25 52-78 BL01052D 10.26 5.737e-25 174-194
800	BL00348	p53 tumor antigen proteins.	BL00348F 23.19 3.714e-09 197-240
801	BL00309	Vertebrate galactoside-binding lectin proteins.	BL00309C 18.65 1.621e-09 62-87
802	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245D 10.47 5.224e-09 187-199
804	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subuni.	PF00774A 16.47 8.457e-10 110-156
808	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667C 11.71 9.875e-09 12-28
810	PD02346	PHOTOSYSTEM II PROTEIN PRECURSOR	PD02346F 12.89 4.340e-09 317-354

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		PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit proteins.	BL00685B 14.41 6.779e-14 54-95 BL00685A 11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PR00080A 9.32 9.419e-10 93-105
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17 22-65
815	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.923e-15 158-171 PD00066 13.92 5.200e-14 46-59 PD00066 13.92 7.000e-14 18-31 PD00066 13.92 7.000e-13 130-143 PD00066 13.92 7.500e-13 214-227 PD00066 13.92 9.000e-13 102-115 PD00066 13.92 4.429e-12 186-199 PD00066 13.92 1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase proteins.	BL01195C 20.12 3.348e-20 100-139
820	BL00520	Interleukin-10 family proteins.	BL00520A 6.21 6.471e-09 1-14
822	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 8.113e-09 224-242
825	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 2.268e-10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN DNA/PANTOTHEN.	PD02855A 18.37 4.732e-28 88-124 PD02855B 8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 7.000e-21 44-62 PR00405C 19.41 1.000e-13 65-87 PR00405A 17.71 7.283e-13 25-45
831	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.000e-09 47-61 PR00019B 11.36 1.720e-09 136-150 PR00019B 11.36 3.880e-09 44-58
832	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.438e-16 164-183 PR00011D 14.03 6.850e-16 164-183 PR00011A 14.06 8.364e-14 164-183 PR00011C 24.25 5.415e-12 231-260 PR00011D 14.03 9.852e-11 212-231
834	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e-12 232-246
835	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 4.000e-10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e-12 216-230
837	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e-09 78-111
839	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 8.302e-09 73-116
840	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 5.091e-22 369-390 PR00700D 12.47 5.765e-21 491-510 PR00700C 13.17 4.750e-14 449-467 PR00700F 11.18 8.500e-

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			11 538-549 PR00700E 17.57 3.100e-10 522-538
841	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.404e-13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.	PD02785B 14.43 1.000e-40 58-112 PD02785A 15.23 1.915e-28 8-57
845	BL00826	MARCKS family proteins.	BL00826C 7.63 6.738e-09 203-230
846	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e-10 15-24
849	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e-08 340-349
850	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 6.506e-09 12-27
851	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 7.000e-16 246-280
852	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e-40 723-778 BL00420B 22.67 1.321e-38 933-988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e-27 587-642 BL00420B 22.67 9.625e-27 270-325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e-23 55-110 BL00420B 22.67 6.464e-20 377-432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e-13 355-366 BL00420C 11.90 1.900e-12 808-819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-11 141-152 BL00420C 11.90 5.119e-11 1018-1029 BL00420C 11.90 7.955e-10 567-578
853	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e-40 756-811 BL00420B 22.67 1.321e-38 966-1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e-27 620-675 BL00420B 22.67 9.625e-27 270-325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e-23 55-110 BL00420B 22.67 6.464e-20 377-432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e-13 355-366 BL00420C 11.90 1.900e-12 841-852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-11 141-152 BL00420C 11.90 5.119e-11 1051-1062 BL00420C 11.90

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			7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 2.778e-09 64-83
859	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 2.929e-13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e-10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e-17 23-41 PR00988C 13.64 8.714e-16 107-123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e-12 176-188 PR00988D 5.95 8.250e-11 163-174 PR00988B 11.60 4.512e-10 60-72
863	BL00215	Mitochondrial energy transfer proteins.	BL00215B 10.44 8.071e-12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775E 8.06 1.000e-24 198-221 PR00775B 3.52 1.837e-23 107-130 PR00775D 8.91 4.484e-17 171-189 PR00775A 9.90 8.342e-17 86-107 PR00775C 10.68 9.379e-17 153-171 PR00775G 10.64 6.850e-15 267-286 PR00775F 12.76 6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e-09 89-121
867	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.596e-29 14-53
868	BL01287	RNA 3'-terminal phosphate cyclase proteins.	BL01287A 17.95 2.688e-26 16-48
869	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e-10 304-337
872	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e-40 30-85
874	BL00188	Biotin-requiring enzymes attachment site proteins.	BL00188 30.29 9.036e-32 665-711
876	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 298-315
877	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 4.176e-10 97-141
879	BL01189	Ribosomal protein S12e proteins.	BL01189A 14.27 1.000e-40 35-71 BL01189B 13.49 1.000e-40 71-125
882	BL00284	Serpins proteins.	BL00284C 28.56 6.400e-25 62-104 BL00284B 17.99 6.182e-12 35-56
889	BL00216	Sugar transport proteins.	BL00216B 27.64 4.375e-21 35-85
896	PR00391	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE	PR00391E 12.50 7.785e-15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e-13 191-207 PR00391A 7.83 5.390e-11 16-36
897	PR00327	ICE NUCLEATION PROTEIN	PR00327C 6.37 5.247e-

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		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 7.800e-26 386-432 BL00039A 18.44 6.674e-16 113-152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e-11 236-260
901	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-16 254-267 PD00066 13.92 8.200e-16 282-295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e-16 366-379 PD00066 13.92 8.200e-16 394-407 PD00066 13.92 8.200e-14 338-351
902	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 9.321e-11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e-09 97-111
904	PR00381	KINESIN LIGHT CHAIN SIGNATURE	PR00381E 8.75 6.586e-25 335-356 PR00381B 18.17 2.667e-24 204-224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e-24 226-245 PR00381D 13.94 1.084e-22 291-309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e-13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e-11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e-09 333-351 PR00381C 12.48 7.120e-09 310-329
906	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e-09 525-549
907	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e-09 513-537
908	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.308e-11 144-155
910	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.800e-30 48-87
912	BL01104	Ribosomal protein L13e proteins.	BL01104C 15.14 6.000e-09 364-392
922	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.842e-09 500-511
923	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.500e-09 323-338 PR00320C 13.01 5.500e-09 187-202
924	PD02181	PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT.	PD02181D 12.85 8.609e-09 36-54
926	BL00019	Actinin-type actin-binding domain proteins.	BL00019C 14.66 7.453e-25 108-144 BL00019B 13.34 6.510e-11 61-84 BL00019D 15.33 9.338e-11 205-235 BL00019A 12.56 2.373e-10 34-45
928	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 9.308e-11

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		proteins proteins.	273-284 BL00678 9.67 1.600e-10 314-325 BL00678 9.67 7.600e-10 360-371 BL00678 9.67 8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.857e-10 137-146
930	BL01085	Ribulose-phosphate 3-epimerase family proteins.	BL01085D 16.55 4.600e-24 134-165 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-20 172-202 BL01085C 21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3-epimerase family proteins.	BLC1085D 16.55 4.600e-24 152-183 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-20 190-220 BL01085C 21.81 2.038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e-09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e-12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-10 5-49
940	PR00862	PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A) SIGNATURE	PR00862D 16.17 4.086e-09 63-84
945	BL01230	RNA methyltransferase trmA family proteins.	BL01230B 11.62 2.373e-09 407-420
948	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 7.429e-18 52-68 BL00479A 19.86 2.200e-13 26-49
949	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.474e-09 100-111
954	PD01311	PROTEIN OXIDOREDUCTASE NAD INTERGENIC RE.	PD01311A 30.23 5.909e-10 66-111
955	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-12 47-60
956	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-12 47-60
957	BL00379	CDP-alcohol phosphatidyltransferases proteins.	BL00379 24.64 1.610e-15 111-148
959	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 1.884e-10 31-75
960	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.438e-14 110-154
962	BL00061	Short-chain dehydrogenases/reductases family proteins.	BL00061B 25.79 6.586e-13 198-236
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e-11 210-225
966	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.035e-09 55-70
967	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 1.286e-12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e-10 73-93 DM01206B 10.69 3.962e-09 108-128 DM01206B 10.69 5.671e-09 38-58
969	PF01008	Initiation factor 2 subunit.	PF01008B 25.59 4.724e-31 417-460 PF01008C 12.25 5.333e-18 506-526 PF01008A 20.14 5.875e-15 369-390

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970	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e-10 112-143 BL01277A 17.39 9.806e-10 40-78
975	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 3.605e-12 130-145 BL01159 13.85 4.122e-10 171-186
977	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791C 20.98 2.235e-09 55-94
978	BL01167	Ribosomal protein L17 proteins.	BL01167B 20.66 8.258e-19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e-13 33-48 BL00478B 14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e-36 169-199 PR00312I 15.78 5.286e-35 332-361 PR00312F 15.06 5.865e-35 199-229 PR00312H 13.31 8.313e-35 263-291 PR00312J 13.73 5.688e-34 363-392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e-33 92-122 PR00312B 15.08 8.941e-33 62-92 PR00312G 11.11 6.657e-32 230-258 PR00312A 11.70 6.914e-27 35-59
981	PF00992	Troponin.	PF00992A 16.67 8.816e-09 414-449
982	PR00299	ALPHA CRYSTALLIN SIGNATURE	PR00299F 13.20 2.367e-09 127-149
983	BL01150	Respiratory-chain NADH dehydrogenase 20 Kd subunit proteins.	BL01150B 17.16 1.000e-40 156-202 BL01150A 14.10 8.200e-39 100-138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e-14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e-10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e-10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e-09 3-48
987	BL00939	Ribosomal protein L1e proteins.	BL00939F 17.27 5.393e-09 810-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-11 525-541
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-11 497-513
994	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e-25 146-189
997	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.893e-11 65-79
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e-09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926C 16.07 1.750e-24 73-94 PR00926D 10.53 3.250e-23 126-145 PR00926F 17.75 6.211e-23 217-240 PR00926E 11.70 6.625e-

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			20 174-193 PR00926B 16.07 2.125e-18 24-39 PR00926A 10.41 1.000e-15 11-25 PR00926F 17.75 5.565e-09 120-143
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e-40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406D 12.58 3.700e-40 270-325 BL00406E 8.44 7.375e-38 327-377 BL00406A 9.95 3.348e-29 11-46
1006	BL00406	Actins proteins.	BL00406B 5.47 1.000e-40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406E 8.44 1.000e-35 248-298 BL00406A 9.95 3.348e-29 11-46
1007	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304D 11.04 8.714e-22 384-407 PR00304C 8.69 4.667e-20 98-118 PR00304B 11.60 7.577e-19 68-87 PR00304A 9.20 3.382e-16 46-63 PR00304E 7.79 6.870e-13 418-431
1009	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.929e-32 9-48
1011	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.929e-32 68-107
1012	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.143e-10 64-73
1016	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168H 12.08 1.000e-11 174-194
1018	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 1.391e-32 261-302 PD00930A 25.62 9.550e-22 157-183
1022	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175A 15.42 5.179e-12 6-26 BL00175C 23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305D 16.34 1.439e-10 158-185
1026	BL00353	HMG1/2 proteins.	BL00353B 11.47 2.436e-18 238-288 BL00353C 14.83 8.844e-11 288-335
1028	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.310e-33 43-91
1033	PF00580	UvrD/REP helicase.	PF00580A 13.37 4.720e-09 111-133
1034	PR00413	HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE	PR00413E 15.78 3.429e-09 154-171
1037	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.657e-09 5-44
1038	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 4.259e-11 55-82
1039	BL00299	Ubiquitin domain proteins.	BL00299 28.84 9.036e-09 17-69
1040	PR00970	ARGININE ADP-RIBOSYLTRANSFERASE	PR00970A 17.73 6.143e-20 56-78 PR00970D

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		SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e-16 224-241 PR00970G 9.97 9.229e-15 242-258 PR00970B 16.37 1.290e-13 86-105 PR00970C 11.05 1.643e-11 115-130 PR00970E 11.23 9.820e-11 202-218
1042	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 243-254
1043	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.786e-13 114-128 PR00048A 10.52 1.000e-09 172-186
1045	BL00615	C-type lectin domain proteins.	BL00615A 16.68 1.720e-11 218-236 BL00615B 12.25 1.857e-10 317-331
1046	BL01092	Adenylate cyclases class-I proteins.	BL01092N 13.54 8.924e-10 3-40
1047	BL01216	ATP-citrate lyase / succinyl-CoA ligases family proteins.	BL01216D 21.75 4.316e-28 314-344 BL01216A 13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e-12 102-136
1050	BL01073	Ribosomal protein L24e proteins.	BL01073 24.30 1.000e-40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e-31 160-212
1055	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 5.235e-11 98-117 BL00030B 7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins domain proteins.	BL00223C 24.79 8.754e-23 262-317 BL00223A 15.59 9.478e-14 46-80 BL00223A 15.59 5.557e-11 118-152
1060	BL00027	'Homeobox' domain proteins.	BL00027 26.43 3.455e-35 158-201
1064	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.211e-13 280-296
1065	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e-09 115-129 PR00019B 11.36 3.880e-09 87-101
1066	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 4.600e-16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e-14 172-191 PR00326D 19.09 1.257e-13 217-236
1071	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 8.518e-11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e-09 350-387
1075	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 4.300e-20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e-11 159-175
1077	PR00724	CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00724A 10.91 1.000e-08 366-379
1078	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 1.000e-12 170-195 BL00215A 15.82 7.529e-10 79-104
1079	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

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		proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e-10 23-57
1094	BL00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e-18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e-12 162-182 BL00460C 14.35 5.500e-09 133-156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e-22 67-105 PD02811B 17.07 2.263e-21 118-151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e-22 60-98 PD02811B 17.07 2.263e-21 111-144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e-09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e-13 111-147
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e-10 15-37 PR00449E 13.50 1.857e-09 185-208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e-20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e-10 63-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1117	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 4.857e-10 290-306
1123	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e-12 301-324
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e-09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis-trans isomerase signatur.	BL00170C 18.49 3.077e-33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e-15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e-15 29-46 BL00636B 15.11 1.360e-14 59-80
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	BL00990C 18.78 4.176e-38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e-27 157-187 BL00990D 16.13 5.320e-18 403-422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e-34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

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			32 159-188 PR00314A 14.53 1.281e-22 13-34
1139	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 6.364e-13 13-57
1141	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.000e-19 451-482 BL00107B 13.31 3.077e-12 519-535
1148	PR00685	TRANSCRIPTION INITIATION FACTOR IIB SIGNATURE	PR00685A 13.62 4.676e-09 21-42
1155	PD01652	RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB.	PD01652B 8.50 9.396e-10 522-574 PD01652B 8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894A 21.96 7.873e-28 81-127 PD02894B 13.93 1.188e-27 178-211
1159	BL00623	GMC oxidoreductases proteins.	BL00623E 15.00 3.531e-20 391-414 BL00623C 10.86 4.240e-20 155-176
1161	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-.	PD01937A 6.68 3.475e-09 330-341
1162	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-.	PD01937A 6.68 3.475e-09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-10 214-239 PR00624D 11.94 1.961e-09 312-337
1167	BL00226	Intermediate filaments proteins.	BL00226B 23.86 7.384e-09 302-350
1177	BL01032	Protein phosphatase 2C proteins.	BL01032G 8.33 1.422e-10 34-48
1178	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 1.794e-10 205-220 PR00320C 13.01 7.840e-10 205-220 PR00320B 12.19 8.457e-10 35-50 PR00320A 16.74 7.146e-09 35-50 PR00320B 12.19 9.100e-09 79-94
1180	PR00454	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-19 765-784
1181	BL00291	Prion protein.	BL00291A 4.49 8.962e-11 152-187
1184	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 4.103e-18 1089-1113
1185	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.553e-13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e-11 104-129
1187	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 2.761e-10 77-93
1188	BL00878	Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si.	BL00878B 10.95 6.000e-16 289-204 BL00878C 17.74 8.435e-15 225-245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e-09 270-289
1191	PD02939	PROTEIN GLUTATHIONE SYNTHETASE SY.	PD02939B 10.10 2.723e-12 203-220 PD02939C 20.01 1.000e-11 224-252
1193	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e-28 72-101 PR00345E

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			8.54 7.652e-28 149-174 PR00345C 4.54 9.100e-28 101-125 PR00345D 10.97 1.964e-24 125-149 PR00345A 13.46 5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e-28 108-137 PR00345E 8.54 7.652e-28 185-210 PR00345C 4.54 9.100e-28 137-161 PR00345D 10.97 1.964e-24 161-185 PR00345A 13.46 5.645e-16 79-98
1195	PF00995	Sec1 family.	PF00995B 17.37 1.120e-13 224-264
1196	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 6.738e-11 15-47
1197	BL01298	Dihydrodipicolinate reductase proteins.	BL01298A 13.90 5.959e-09 51-73
1203	BL00061	Short-chain dehydrogenases/reductases family proteins.	BL00061B 25.79 1.000e-14 152-190
1204	PR00118	BETA-LACTAMASE CLASS A SIGNATURE	PR00118F 16.42 9.386e-09 213-229
1206	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 1.429e-37 184-229 BL01183D 27.71 8.535e-27 264-307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e-09 246-258
1208	BL00979	G-protein coupled receptors family 3 proteins.	BL00979L 20.63 2.485e-09 105-146
1209	PF00023	Ank repeat proteins.	PF00023A 16.03 4.857e-11 49-65 PF00023B 14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e-14 227-241 PR00048A 10.52 4.316e-11 199-213
1213	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.720e-10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e-09 44-64
1216	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.598e-10 179-230
1219	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.348e-11 249-264
1222	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e-15 295-308 PD00066 13.92 7.231e-15 406-419 PD00066 13.92 2.286e-12 378-391 PD00066 13.92 7.857e-12 434-447 PD00066 13.92 3.348e-11 350-363
1223	BL50058	G-protein gamma subunit profile.	BL50058 27.23 1.000e-40 13-61
1226	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.439e-09 279-330
1227	BL00437	Catalase proximal heme-ligand proteins.	BL00437A 18.82 1.000e-40 49-101 BL00437B 16.28 1.000e-40 114-168 BL00437C 21.86

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			1.000e-40 190-239 BL00437D 25.72 1.000e-40 248-301 BL00437E 23.95 1.000e-40 327-379
1230	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 8.297e-10 6-60
1231	PR00735	GLYCOSYL HYDROLASE FAMILY 8 SIGNATURE	PR00735A 11.19 6.857e-09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e-10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e-10 158-176
1235	BL00866	Carbamoyl-phosphate synthase subdomain proteins.	BL00866B 36.29 2.776e-09 75-121
1237	BL00027	'Homeobox' domain proteins.	BL00027 26.43 1.818e-21 36-79
1243	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e-11 10-25
1246	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168L 9.47 2.837e-10 31-46 PD01168L 9.47 4.490e-10 174-189 PD01168L 9.47 7.612e-10 183-198
1249	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.800e-10 183-196
1254	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 2.440e-36 96-144
1255	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e-11 8-52
1256	BL00373	Phosphoribosylglycinamide formyltransferase proteins.	BL00373C 10.35 3.348e-12 143-156
1258	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.217e-10 174-193
1259	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 8.286e-10 31-40
1261	PR00070	DIHYDROFOLATE REDUCTASE SIGNATURE	PR00070D 11.63 1.000e-15 112-127 PR00070C 13.09 9.500e-15 51-63 PR00070A 12.92 5.500e-12 16-27
1262	BL00462	Gamma-glutamyltranspeptidase proteins.	BL00462A 20.89 6.438e-24 140-183 BL00462B 17.88 5.500e-20 230-267 BL00462C 27.41 2.023e-11 292-347
1263	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 9.455e-11 62-83
1264	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e-11 17-61
1266	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 2.714e-18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e-12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 9.308e-22 40-63 PR00449E 13.50 1.000e-16 137-160 PR00449D 10.79 3.520e-11 102-116
1270	BL00276	Channel forming colicins proteins.	BL00276A 8.87 1.500e-09 17-29
1275	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327C 15.47 9.769e-09 228-243
1276	PR00412	EPOXIDE HYDROLASE	PR00412B 12.59 7.894e-

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		SIGNATURE	12 119-135 PR00412C 11.30 1.857e-11 165-179 PR00412A 13.23 3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.538e-10 127-157
1279	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e-13 128-145
1280	BL01220	Phosphatidylethanolamine -binding protein family proteins.	BL01220C 14.75 9.348e-15 248-276
1285	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.286e-10 33-42
1287	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.182e-11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY SIGNATURE	PR00802B 16.51 1.610e-10 81-105
1297	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE	PR00716C 17.65 5.696e-09 23-44
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e-14 268-283
1301	BL00127	Pancreatic ribonuclease family proteins.	BL00127C 31.49 3.571e-28 82-126 BL00127B 26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR SIGNATURE	PR00637E 11.27 4.250e-09 290-306
1307	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.500e-17 13-38 BL00215A 15.82 1.000e-16 226-251 BL00215A 15.82 2.658e-13 107-132
1308	PR00898	VASOPRESSIN V2 RECEPTOR SIGNATURE	PR00898H 11.34 4.682e-09 552-572
1309	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 2.731e-09 390-401
1310	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 9.654e-13 73-89 BL00983B 8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family proteins.	BL00194 12.16 1.900e-11 15-28
1314	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 8.969e-10 53-97
1316	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e-13 128-145
1320	BL00783	Ribosomal protein L13 proteins.	BL00783C 22.43 6.559e-24 87-117 BL00783A 14.55 1.600e-19 8-33 BL00783B 12.76 3.500e-12 74-86
1327	PF00514	Armadillo/beta-catenin-like repeat proteins.	PF00514A 31.30 7.268e-11 82-120
1329	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.294e-11 129-148 BL00030B 7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 7.239e-09 25-43
1332	PR00161	NICKEL-DEPENDENT HYDROGENASE/B-TYPE CYTOCHROME SIGNATURE	PR00161C 9.51 4.930e-09 317-337
1333	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 6.769e-33 10-49
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e-09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

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		PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e-13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e-16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e-21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e-09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e-10 135-146
1348	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 7.231e-13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e-32 416-445 PR00193C 12.60 6.318e-31 179-207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e-22 470-499 PR00193A 15.41 1.783e-20 77-97
1352	PR00447	NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	PR00447E 9.73 1.554e-15 299-319 PR00447D 13.54 3.408e-15 200-224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e-10 353-373
1353	BL00303	S-100/ICaBP type calcium binding protein.	BL00303A 21.77 6.667e-26 45-82 BL00303B 26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 5.950e-29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e-18 225-249 BL00039B 19.19 3.182e-14 141-167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e-12 84-101 PF00615C 10.06 8.412e-12 162-176
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.234e-29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e-18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e-12 53-64 PR00925D 6.56 1.857e-10 76-87
1362	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e-30 136-171 BL01272C 11.68 3.314e-25 249-274 BL01272A 6.49 1.231e-18 99-117
1363	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e-30 113-148 BL01272C 11.68 3.314e-25 226-251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	W KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e-09 167-177
1368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e-09 76-96
1370	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 1.794e-

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			10 1-19
1371	BL00242	Integrins alpha chain proteins.	BL00242B 8.13 8.615e-09 469-479
1372	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625B 13.48 7.353e-19 46-67 PR00625A 12.84 1.391e-16 14-34
1373	BL00434	HSF-type DNA-binding domain proteins.	BL00434C 23.85 3.778e-09 90-130
1374	PR00962	LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE	PR00962C 8.00 6.337e-09 505-526
1375	PD02475	MUCIN EPITHELIAL TUMOR-ASSOCIATE.	PD02475A 23.18 8.552e-10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.571e-32 24-63
1380	BL00194	Thioredoxin family proteins.	BL00194 12.16 8.333e-12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 1.458e-15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 243-254
1384	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 271-282
1385	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 6.203e-10 95-132
1386	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e-09 1574-1628
1387	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e-11 52-61
1389	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.600e-30 10-49
1390	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.512e-31 32-71
1392	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 9.723e-10 127-137
1393	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.625e-25 88-110 PR00380D 9.93 2.406e-20 304-326 PR00380B 12.64 4.414e-16 208-226 PR00380C 13:18 6.538e-16 243-262
1394	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e-14 462-475 PD00066 13.92 8.800e-14 348-361 PD00066 13.92 9.571e-12 405-418 · PD00066 13.92 6.087e-11 490-503 PD00066 13.92 8.043e-11 320-333
1398	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 6.786e-32 10-49
1400	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.038e-09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 7.324e-15 363-389
1407	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.500e-10 457-476
1408	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.550e-11 179-193 PR00019A 11.19 8.826e-10 228-242 PR00019B 11.36 1.360e-09 199-213 PR00019B 11.36 4.960e-

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			09 176-190
1409	PR00510	NEBULIN SIGNATURE	PR00510A 9.09 4.150e-12 182-202 PR00510B 12.96 8.767e-12 210-230 PR00510F 9.88 8.172e-10 58-75 PR00510D 9.21 2.367e-09 251-267
1410	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.696e-09 31-44
1412	BL00358	Ribosomal protein L5 proteins.	BL00358B 22.76 1.00Ce-40 57-103 BL00358C 13.75 6.087e-14 122-136 BL00358D 14.26 5.500e-13 143-158 BL00358A 13.06 1.931e-11 33-44
1414	BL00282	Kazal serine protease inhibitors family proteins.	BL00282 16.88 7.338e-10 511-534
1415	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 4.300e-29 40-77
1417	PR00681	RIBOSOMAL PROTEIN S1 SIGNATURE	PR00681G 12.54 2.149e-09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.462e-09 171-208
1419	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 1.571e-09 428-443
1420	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941A 14.81 1.000e-40 142-196 PD01941B 15.02 7.049e-30 400-447 PD01941E 15.92 2.475e-20 817-864 PD01941C 19.96 3.118e-19 488-543 PD01941D 27.18 9.614e-18 641-690 PD01941F 28.52 5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e-12 199-217
1423	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 6.318e-11 1009-1028
1424	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 8.200e-14 367-386 BL50002A 14.19 9.250e-12 298-317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e-09 244-258
1425	PF00628	PHD-finger.	PF00628 15.84 3.045e-12 330-345
1426	PF00628	PHD-finger.	PF00628 15.84 3.045e-12 377-392
1427	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.114e-16 281-299 PR00405A 17.71 4.306e-14 262-282
1428	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 5.219e-34 147-193
1429	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.920e-10 577-592
1430	PR00378	INOSITOL PHOSPHATASE SIGNATURE	PR00378D 16.86 7.563e-12 295-314 PR00378B 13.80 8.650e-10 166-186
1431	PR00928	GRAVES DISEASE CARRIER	PR00928B 13.53 3.769e-

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		PROTEIN SIGNATURE	10 103-124
1433	BL01113	C1q domain proteins.	BL01113B 18.26 7.049e-15 14-50 BL01113C 13.18 7.000e-12 82-102
1434	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 7.983e-10 135-150
1436	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 1.000e-12 84-103
1438	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.500e-09 250-268 BL00290A 20.89 4.000e-09 188-211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-09 38-52
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-09 88-102
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e-08 114-138
1445	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e-40 73-123 PD01841B 14.35 1.000e-40 144-185 PD01841D 17.87 1.000e-40 206-258 PD01841F 13.36 1.000e-40 296-345 PD01841G 24.26 1.000e-40 349-403 PD01841I 23.00 1.000e-40 494-536 PD01841J 14.94 1.000e-40 895-932 PD01841L 18.42 1.000e-40 1083-1125 PD01841E 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e-35 1041-1071 PD01841H 21.30 3.189e-31 435-472 PD01841C 13.78 1.000e-25 185-206 PD01841M 10.82 1.250e-20 1175-1194
1446	PF00816	H-NS histone family.	PF00816B 13.84 8.875e-09 190-220
1447	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.080e-09 402-416
1448	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315D 18.40 7.393e-09 23-67
1451	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 2.800e-10 94-104
1454	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 7.146e-09 382-405
1455	PF00777	Sialyltransferase family.	PF00777C 18.60 2.929e-22 4-59
1457	BL00927	Trehalase proteins.	BL00927C 10.83 8.085e-09 42-53
1460	BL00545	Aldose 1-epimerase proteins.	BL00545C 11.28 7.353e-17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e-09 140-153
1466	PR00097	ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE	PR00097C 9.42 9.069e-09 233-245
1472	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 5.250e-22 170-195 BL01129C 25.56 9.526e-18 63-106
1473	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e-09 2114-2145
1475	PF00686	Starch binding domain proteins.	PF00686A 13.45 9.100e-09 267-277

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1477	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e-10 466-476
1478	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 9.400e-10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10 292-305
1480	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.385e-15 69-87 BL00290A 20.89 5.091e-11 12-35
1481	PR00150	PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE	PR00150F 10.45 9.039e-09 21-51
1482	PF00780	Domain found in NIK1-like kinases, mouse citron and yeast ROM.	PF00780I 14.69 4.825e-09 107-137
1483	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e-09 108-162
1485	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.909e-25 17-56
1486	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.529e-09 34-50
1488	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 9.586e-10 116-162
1490	BL00166	Enoyl-CoA hydratase/isomerase proteins.	BL00166D 22.87 2.607e-24 190-226 BL00166C 18.93 5.500e-14 140-167 BL00166B 16.92 9.357e-11 93-115
1491	BL00452	Guanylate cyclases proteins.	BL00452D 28.59 3.700e-31 63-106 BL00452E 11.92 3.045e-13 115-131
1492	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 3.667e-09 532-546
1497	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-11 384-400 BL00107A 18.39 5.345e-11 322-353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e-10 107-117
1502	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e-24 112-155
1503	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e-24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 5.800e-24 448-475 BL01177C 17.39 5.333e-19 402-421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e-15 427-445
1506	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 5.500e-14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e-10 341-363
1512	BL00523	Sulfatases proteins.	BL00523E 19.27 4.536e-22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e-09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 7.045e-14 168-218
1518	BL00600	Aminotransferases class-III pyridoxal-phosphate attachment si.	BL00600A 17.98 6.143e-19 98-122 BL00600E 16.43 1.771e-17 302-

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			331 BL00600G 12.43 9.625e-17 377-396 BL00600B 19.60 5.091e-15 160-186 BL00600C 16.18 6.040e-12 190-206 BL00600F 8.77 1.000e-11 343-356 BL00600D 8.71 1.000e-10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 9.600e-18 41-82
1528	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 4.774e-11 192-207 PR00320B 12.19 8.839e-11 272-287 PR00320B 12.19 9.743e-10 106-121 PR00320A 16.74 1.878e-09 192-207 PR00320A 16.74 2.317e-09 106-121 PR00320A 16.74 8.683e-09 272-287 PR00320C 13.01 8.800e-09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 4.508e-15 171-184
1539	PF00781	Diacylglycerol kinase catalytic domain proteins (presumed).	PF00781D 11.11 7.593e-10 103-127
1540	PR00965	OCULAR ALBINISM TYPE 1 PROTEIN SIGNATURE	PR00965H 10.73 1.231e-29 312-334 PR00965E 12.93 5.846e-29 172-195 PR00965F 5.98 1.123e-28 209-231 PR00965C 15.04 1.000e-27 131-151 PR00965D 5.84 1.000e-27 150-170 PR00965G 8.52 2.440e-27 258-279 PR00965B 4.80 8.650e-26 88-109 PR00965A 12.52 1.000e-25 35-55 PR00965I 3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 9.719e-17 163-207
1543	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699C 24.84 1.000e-40 599-646 PD02699A 8.91 2.286e-34 219-248 PD02699B 18.28 6.143e-21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.857e-10 182-197 PR00049D 0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein retaining receptor proteins.	BL00951C 19.35 1.000e-40 93-142 BL00951D 13.94 8.714e-40 142-177 BL00951A 15.10 1.000e-38 2-38 . BL00951B 14.23 6.250e-33 38-69
1548	BL00536	Ubiquitin-activating enzyme proteins.	BL00536F 13.65 8.920e-30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e-18 248-279
1549	PR00139	ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE	PR00139C 11.72 9.679e-09 550-569
1553	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.119e-09 58-73

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1556	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.276e-13 67-105
1557	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-12 107-132
1558	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-12 107-132
1559	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-12 107-132
1562	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 6.600e-18 412-436 BL00522B 27.30 1.738e-16 364-410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e-14 502-532 BL00522F 14.90 2.385e-13 551-575
1563	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 1.947e-11 46-59
1564	BL00299	Ubiquitin domain proteins.	BL00299 28.84 2.823e-10 324-376
1566	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 8.594e-17 184-228 BL01013C 9.97 4.906e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10 295-306
1570	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 5.235e-17 297-313 BL00479A 19.86 6.625e-15 271-294 BL00479A 19.86 2.667e-14 147-170 BL00479B 12.57 6.294e-12 173-189
1576	PR00665	OXYTOCIN RECEPTOR SIGNATURE	PR00665G 12.36 4.673e-24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e-22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e-19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e-15 11-25
1577	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 9.308e-10 127-137
1579	BL00524	Somatomedin B domain proteins.	BL00524A 9.65 6.776e-14 52-73
1580	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894B 13.93 6.959e-16 182-215 PD02894A 21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain proteins.	BL00411C 15.04 5.292e-12 32-54 BL00411H 15.66 4.441e-11 245-276
1582	PR00604	CLASS IA AND IB CYTOCHROME C SIGNATURE	PR00604A 11.13 2.440e-09 79-87
1584	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 1.000e-10 225-238
1585	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551C 14.62 9.455e-11 125-145
1586	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354S 11.61 7.750e-09 474-495

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1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e-33 180-210 PR00072A 12.75 6.040e-25 120-145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e-22 276-295 PR00072E 10.54 1.360e-19 301-318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e-15 332-349
1589	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191H 15.64 1.537e-22 61-113 BL00191K 17.38 9.027e-12 398-442
1590	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e-13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1 CHROMOSOME.	DM00517B 10.96 6.625e-16 1175-1193 DM00517A 8.21 1.000e-11 1015-1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e-27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e-12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e-10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e-09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e-11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e-09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e-10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e-10 136-187
1605	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.571e-10 44-57
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e-23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e-08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.98 7.353e-10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e-09 365-391
1613	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e-09 932-983 BL00412D 16.54 7.153e-09 933-984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 3.531e-25 54-83 BL00559K 13.17 2.957e-18 197-224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e-16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e-22 500-541 PD01427A 19.94 8.773e-18 439-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RRSULTS*
			472
1616	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 7.485e-09 152-201 BL00115Z 3.12 9.603e-09 145-194
1617	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 7.750e-32 51-88 BL00303A 21.77 1.947e-31 4-41
1618	BL01254	Fetuin family proteins.	BL01254F 10.02 8.754e-09 137-147
1619	PD01888	PEPTIDE REDUCTASE PROTEIN METHI.	PD01888B 25.10 1.000e-40 47-97 PD01888C 21.56 7.000e-30 125-155 PD01888A 12.84 8.800e-15 7-23
1621	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 3.455e-09 692-704 PR00239E 1.58 4.580e-09 697-709 PR00239E 1.58 4.580e-09 702-714 PR00239E 1.58 5.193e-09 703-715
1622	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860B 7.04 1.900e-18 27-41 PR00860C 9.61 1.474e-14 41-51 PR00860A 5.46 1.720e-14 5-18
1624	PR00784	MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE	PR00784D 15.86 8.027e-11 77-95
1626	BL00325	Actin-depolymerizing proteins.	BL00325B 21.66 1.000e-40 93-139 BL00325A 24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase proteins.	BL00064B 23.57 1.000e-40 82-130 BL00064C 17.28 1.000e-40 137-182 BL00064E 27.20 1.000e-40 223-275 BL00064F 25.14 7.882e-36 286-331 BL00064A 21.16 1.000e-33 22-60 BL00064D 14.19 6.500e-31 182-212
1632	PR00063	RIBOSOMAL PROTEIN L27 SIGNATURE	PR00063B 15.24 9.700e-11 59-84 PR00063A 11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239D 0.00 1.105e-11 36-49 PR00239C 3.51 2.538e-09 37-45
1636	BL01210	Caveolins proteins.	BL01210B 13.92 9.531e-10 133-183
1637	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 5.388e-11 11-43
1639	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 8.144e-12 132-177
1640	PR00015	GRAM-POSITIVE COCCUS SURFACE PROTEIN ANCHOR SIGNATURE	PR00015B 9.84 8.468e-10 128-149
1641	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 5.935e-11 364-379 PR00320A 16.74 7.828e-11 364-379 PR00320C 13.01 2.800e-10 279-294 PR00320C 13.01 2.800e-10 364-379 PR00320B 12.19 5.114e-10 279-294 PR00320A 16.74 1.659e-09 279-294

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00320A 16.74 2.098e-09 229-244
1642	PF00023	Ank repeat proteins.	PF00023A 16.03 6.464e-09 114-130
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e-11 74-94
1644	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e-17 56-89
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.270e-21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e-16 332-351 PR00380B 12.64 6.657e-15 292-310
1647	DM01242	3 THREONINE--TRNA LIGASE.	DM01242C 17.15 9.791e-37 340-381 DM01242E 23.00 5.071e-31 463-505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e-18 265-314 DM01242F 10.61 7.618e-14 526-540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e-10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e-11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e-12 11-35 BL00933E 13.80 9.217e-09 456-472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e-10 70-115
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e-17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e-17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e-16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e-11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e-10 442-455
1659	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e-12 376-401 BL00972E 20.72 5.629e-09 446-468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e-15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e-13 1140-1157 PR00105B 12.32 2.800e-12 1259-1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e-33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e-19 51-68 PR00319B 11.47 8.200e-19 70-85

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1664	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.050e-10 489-502
1667	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.500e-38 7-46
1669	BL01153	NOL1/NOP2/sun family proteins.	BL01153D 19.69 1.188e-17 115-141 BL01153C 13.67 8.977e-15 66-80 BL01153B 20.52 1.885e-10 13-37
1671	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 3.100e-10 1146-1169
1672	BL00598	Chromo domain proteins.	BL00598 14.45 8.500e-20 27-49
1673	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.329e-09 686-707
1674	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.580e-11 343-358 PR00049D 0.00 1.286e-10 342-357
1676	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e-19 427-448 PR00747G 14.50 2.286e-18 368-393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747D 15.23 8.759e-17 163-183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 311-328
1677	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e-19 309-330 PR00747G 14.50 2.286e-18 250-275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 193-210
1680	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331
1681	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 329-340 BL00678 9.67 6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 1.346e-13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR SIGNATURE	PR00646H 6.32 4.188e-09 755-771
1690	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e-09 75-129
1691	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.281e-10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e-10 420-435
1692	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.281e-10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-10 489-504
1693	BL00674	AAA-protein family proteins.	BL00674C 22.60 8.043e-24 274-317 BL00674B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			4.46 4.000e-23 241-263 BL00674D 23.41 8.560e-18 338-385 BL00674E 15.24 1.720e-15 414-434
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e-10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466C 10.17 3.443e-13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e-09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e-12 283-300 BL00028 16.07 3.769e-11 255-272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e-11 227-244 BL00028 16.07 1.600e-10 199-216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e-15 62-102 BL01019B 19.49 4.000e-15 107-162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.484e-12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558e-14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.565e-10 116-130 PR00019B 11.36 4.600e-09 113-127 PR00019B 11.36 7.120e-09 204-218
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e-11 232-247 BL01159 13.85 5.408e-10 613-628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e-10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e-11 230-241
1714	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e-11 230-241
1715	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 7.129e-09 7-51
1718	BL00353	HMG1/2 proteins.	BL00353C 14.83 6.018e-10 136-183 BL00353B 11.47 8.866e-09 86-136
1719	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.408e-09 432-483
1721	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 8.448e-12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e-09 418-428
1724	BL01279	Protein-L-isoaspartate(D-aspartate) O-methyltransferase signa.	BL01279A 24.27 5.663e-12 233-281
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41 4.176e-11 157-170
1730	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 1.089e-09 17-61

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1731	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e-10 296-350
1732	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e-10 316-370
1733	PF00850	Histone deacetylase family.	PF00850F 15.70 4.349e-22 246-279 PF00850D 14.76 6.850e-20 177-201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e-14 281-323
1734	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354C 6.61 5.932e-09 292-307
1735	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.263e-10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167
1744	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167
1745	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 8.297e-15 136-160
1746	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.727e-11 45-57 PR00081E 17.54 3.935e-10 150-168
1747	BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	BL00439H 18.24 8.435e-14 65-91 BL00439G 13.40 2.895e-12 3-14
1749	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 7.158e-11 4-20
1751	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e-14 33-46 PD00066 13.92 1.000e-13 89-102 PD00066 13.92 7.000e-13 61-74 PD00066 13.92 6.571e-12 117-130
1753	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 6.516e-18 33-77
1754	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.393e-09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e-09 287-318
1756	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.750e-35 10-49
1758	DM00406	GLIADIN.	DM00406 7.73 7.600e-09 653-666
1762	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 4.529e-09 224-278
1765	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.950e-11 146-167
1775	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e-14 523-539
1776	BL00942	glpT family of transporters proteins.	BL00942F 15.07 4.343e-10 371-389 BL00942B 20.36 8.040e-09 94-137
1777	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e-09 279-312

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e-20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e-11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e-18 611-655 BL01013A 25.14 2.881e-15 344-380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e-12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e-13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e-13 492-515

* results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TRADOCS:1416223.1(%CRJ01!.DOC)

TABLE 4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
2	ig	Immunoglobulin domain	2.1e-32	109.5
3	pkinase	Eukaryotic protein kinase domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	0	1090.4
8	fn3	Fibronectin type III domain	0	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	35.4
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP_GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH_C	IMP dehydrogenase / GMP reductase C terminus	1.6e-119	410.5
21	IMPDH_C	IMP dehydrogenase / GMP reductase C terminus	4.3e-102	352.6
22	pkinase	Eukaryotic protein kinase domain	2.4e-79	277.0
23	pkinase	Eukaryotic protein kinase domain	8.4e-74	258.6
25	RNA_pol_A	RNA polymerase alpha subunit	0	1077.7
26	C1q	C1q domain	1.9e-10	44.4
27	Ribosomal_L23	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L23	Ribosomal protein L23	1e-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	Ets	Ets-domain	1.4e-56	182.1
45	Ets	Ets-domain	1.4e-56	182.1
46	LRR	Leucine Rich Repeat	1.7e-13	58.3
48	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
49	ITAM	Immunoreceptor tyrosine-based activation mot	1.4e-05	31.9
50	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
52	ras	Ras family	8.5e-45	162.3
53	PRK	Phosphoribulokinase	2.1e-65	230.7
54	myb_DNA-binding	Myb-like DNA-binding domain	0.096	15.2
55	voltage_CLC	Voltage gated chloride channels	3.3e-186	631.9
56	sugar_tr	Sugar (and other) transporter	0.00015	-64.3
57	TBC	TBC domain	2.2e-37	137.6
58	ank	Ank repeat	5.9e-25	96.3
59	ank	Ank repeat	5.9e-25	96.3
67	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	7.9e-49	175.6
68	C2	C2 domain	7.9e-54	192.2
69	C2	C2 domain	2.3e-54	194.0
70	Kelch	Kelch motif	9.4e-99	341.5
72	ig	Immunoglobulin domain	8.2e-28	94.7
73	pkinase	Eukaryotic protein kinase	8e-69	242.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
		domain		
74	pkinase	Eukaryotic protein kinase domain	2.8e-38	140.6
76	zf-C4_Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase_S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92	laminin_G	Laminin G domain	6.1e-27	98.5
93	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
95	pkinase	Eukaryotic protein kinase domain	1.4e-59	211.4
96	pkinase	Eukaryotic protein kinase domain	2.6e-51	183.9
97	adh_short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various cellular act	6.8e-05	-5.2
104	pkinase	Eukaryotic protein kinase domain	2.7e-73	256.9
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductase	FAD/NAD-binding Cytochrome reductase	7.7e-61	215.5
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
116	PH	PH domain	3.1e-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty-acid binding pr	2.4e-14	53.5
118	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
120	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5_eIF4_eIF2	eIF4-gamma/eIF5/eIF2-epsilon	1e-32	122.2
124	ig	Immunoglobulin domain	6.5e-08	30.6
127	mito_carr	Mitochondrial carrier proteins	3e-16	58.6
128	PP2C	Protein phosphatase 2C	2.2e-71	250.6
129	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	3.1e-20	80.6
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133	ACBP	Acyl CoA binding protein	4.6e-22	86.7
134	rrm	RNA recognition motif.	1.2e-31	118.5
135	IQ	IQ calmodulin-binding motif	2.6e-08	41.0
136	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	9.3e-22	85.7
139	WH2	Wiskott Aldrich syndrome homology region 2	0.0067	23.1
140	zf-C2H2	Zinc finger, C2H2 type	1.7e-82	287.5
141	Peptidase_S26	Signal peptidase I	5.7e-10	35.7
143	arf	ADP-ribosylation factor family	1.2e-39	145.2
146	KRAB	KRAB box	7.3e-30	112.6
148	DUF6	Integral membrane protein DUF6	0.096	8.0
149	PDEase	3'5'-cyclic nucleotide phosphodiesterase	3.8e-80	231.1
151	S4	S4 domain	1.1e-08	42.3
153	tRNA-synt_1d	tRNA synthetases class I (R)	3.8e-103	356.1
154	Cyt_reductase	FAD/NAD-binding Cytochrome reductase	7.8e-60	212.2
155	ras	Ras family	3.6e-28	107.0
157	actin	Actin	3.8e-26	87.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
160	Zn_carbOpept	Zinc carboxypeptidase	5e-138	471.9
165	pkinase	Eukaryotic protein kinase domain	5.1e-67	236.1
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	27.0
168	Ribosomal_S15	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	1e-48	157.0
171	DUF59	Domain of unknown function DUF59	0.07	-17.4
172	pkinase	Eukaryotic protein kinase domain	3.7e-15	58.6
173	globin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	1e-31	118.8
178	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	2.5e-17	71.0
179	zf-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	C1q	C1q domain	8.8e-72	251.9
190	Y_phosphatase	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase domain	6.5e-82	285.6
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent enzyme	2.5e-64	227.1
197	DnaJ	DnaJ domain	1.6e-38	141.4
199	RrnaAD	Ribosomal RNA adenine dimethylases	0.00018	16.9
200	acid_phospha t	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP-synt_AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	vATP-synt_AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	C1q	C1q domain	1.6e-70	247.7
212	UQ_con	Ubiquitin-conjugating enzyme	7.4e-74	258.8
213	UQ_con	Ubiquitin-conjugating enzyme	1e-53	191.9
215	DEAD	DEAD/DEAH box helicase	1.8e-43	140.4
216	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos_transf_2	Glycosyl transferases	4e-21	83.6
219	ig	Immunoglobulin domain	0.092	10.7
222	WD40	WD domain, G-beta repeat	7.4e-23	89.4
224	TPR	TPR Domain	1.2e-08	42.1
225	DnaJ_CXXCXGXG	DnaJ central domain (4 repeats)	1.5e-38	141.5
226	DnaJ_CXXCXGXG	DnaJ central domain (4 repeats)	1.5e-38	141.5
229	HSP70	Hsp70 protein	2.4e-54	194.0
230	GSHPx	Glutathione peroxidases	3.4e-47	170.2
231	tsp_1	Thrombospondin type 1 domain	0.0075	17.1
233	cyclin	Cyclin	4.6e-144	492.0
234	ras	Ras family	4.8e-50	179.7
235	LRR	Leucine Rich Repeat	1.2e-30	115.3
236	LRR	Leucine Rich Repeat	6.7e-29	109.4
237	PDZ	PDZ domain (Also known as DHR or GLGF).	1.7e-09	45.0

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
244	dCMP_cyt_deam	Cytidine and deoxycytidylate deaminase	2.5e-05	31.1
245	ig	Immunoglobulin domain	6.7e-08	30.5
248	wnt	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito_carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekinase	Adenylate kinase	1.8e-14	55.7
255	Cation_efflux	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid transporter protein	2.6e-52	187.2
258	adenylatekinase	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial_PQQ	PQQ enzyme repeat	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kinase	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal_S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase domain	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_transf_4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	2e-44	161.0
306	rrm	RNA recognition motif.	2.7e-44	160.6
308	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA_polymeraseX	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.1e-60	192.3
315	Kelch	Kelch motif	1.3e-106	367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	ARID DNA binding domain	5.1e-37	136.4
327	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
328	cadherin	Cadherin domain	8.1e-81	281.9
331	chromo	'chromo' (CHRromatin Organization MOdifier)	4e-18	66.7
333	Peptidase_M22	Glycoprotease family	1.2e-136	467.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
335	vwa	von Willebrand factor type A domain	2.3e-07	37.9
339	ras	Ras family	7.8e-07	-59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	ig	Immunoglobulin domain	0.0005	18.0
346	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.1e-15	63.3
355	PHD	PHD-finger	3.2e-07	37.4
358	DUF6	Integral membrane protein DUF6	0.033	15.8
359	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	79.4
361	ank	Ank repeat	6.6e-34	126.1
362	ArfGap	Putative GTP-ase activating protein for Arf	4.7e-53	189.7
363	efhand	EF hand	5.4e-10	46.6
367	LRR	Leucine Rich Repeat	8.8e-44	158.9
368	laminin_G	Laminin G domain	1.5e-33	121.7
369	PP2C	Protein phosphatase 2C	5.3e-20	73.9
372	LIM	LIM domain containing proteins	9.9e-15	57.1
373	KRAB	KRAB box	4.8e-23	90.0
376	ion_trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase domain	1.6e-94	327.5
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin-transferase).	1.3e-07	-13.5
384	ank	Ank repeat	2.5e-101	350.0
386	ig	Immunoglobulin domain	9.5e-05	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito_carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.1e-21	83.6
396	spectrin	Spectrin repeat	2.1e-67	237.3
397	zf-C2H2	Zinc finger, C2H2 type	0.0066	23.1
399	fn3	Fibronectin type III domain	4.1e-102	352.6
400	WD40	WD domain, G-beta repeat	0.00049	26.8
401	E1_dehydrog	Dehydrogenase E1 component	3e-119	409.6
402	fn3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGEF	RhoGEF domain	1.1e-23	92.1
411	F-box	F-box domain.	4.2e-06	33.7
412	SNF2_N	SNF2 and others N-terminal domain	5.8e-16	61.6
415	CPSase_L_chain	Carbamoyl-phosphate synthase (CPSase)	1.5e-172	586.6
418	LRR	Leucine Rich Repeat	3.8e-24	93.6
419	DENN	DENN (AEX-3) domain	2e-58	207.5
420	RasGEF	RasGEF domain	8.1e-43	155.7
421	ank	Ank repeat	1.4e-153	523.7
424	G-patch	G-patch domain	1e-19	78.9
425	pkinase	Eukaryotic protein kinase domain	2.2e-31	117.1
426	Plexin_repeat	Plexin repeat	0.0023	24.6
427	Plexin_repea	Plexin repeat	0.0023	24.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	t			
429	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	8.6e-11	39.2
431	DEAD	DEAD/DEAH box helicase	1e-66	214.0
432	SH3	SH3 domain	3.4e-16	67.2
433	GTP_CDC	Cell division protein	2.1e-114	393.5
436	Collagen	Collagen triple helix repeat (20 copies)	4.6e-194	658.1
438	Ricin_B_lect in	Similarity to lectin domain of ricin b	0.0085	10.5
441	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	1.2e-256	866.0
442	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	1.8e-235	795.7
443	PDZ	PDZ domain (Also known as DHR or GLGF).	1.9e-65	230.9
445	LON	ATP-dependent protease La (LON) domain	0.00012	-17.1
446	ig	Immunoglobulin domain	0.00011	20.1
451	sushi	Sushi domain (SCR repeat)	1.4e-18	75.2
452	fn3	Fibronectin type III domain	1.5e-06	35.2
454	pyridoxal_de C	Pyridoxal-dependent decarboxylase conse	8.3e-14	50.3
456	kinesin	Kinesin motor domain	4.9e-217	734.4
457	neur_chan	Neurotransmitter-gated ion-channel	1e-175	597.1
458	Josephin	Josephin	0.0002	18.7
468	bZIP	bZIP transcription factor	1.7e-07	31.8
470	NTP_transfer ase	Nucleotidyl transferase	6.3e-06	-26.3
471	WD40	WD domain, G-beta repeat	2e-28	107.9
473	LIM	LIM domain containing proteins	0.00021	20.7
477	zf-RanBP	Zn-finger in Ran binding protein and others.	0.028	21.0
479	WD40	WD domain, G-beta repeat	6.5e-18	73.0
480	KRAB	KRAB box	1e-31	118.8
481	ArfGap	Putative GTP-ase activating protein for Arf	8.4e-66	232.0
485	SH2	Src homology domain 2	0.011	11.4
486	C1q	C1q domain	4.3e-74	259.6
487	dsrm	Double-stranded RNA binding motif	1.1e-47	171.9
489	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
490	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	3.4e-222	751.6
492	SKI	Shikimate kinase	1.2e-10	48.8
497	ENV_polyprot ein	ENV polyprotein (coat polyprotein)	2.6e-22	77.6
498	abhydrolase_ 2	Phospholipase/Carboxylesterase	0.041	-48.1
500	rrm	RNA recognition motif.	5.4e-34	126.4
501	WW	WW domain	4.6e-18	73.4
502	ig	Immunoglobulin domain	1.1e-10	39.5
504	abhydrolase	alpha/beta hydrolase fold	0.045	-3.6
505	vwa	von Willebrand factor type A domain	7.1e-62	219.0
508	Na_K_ATPase_ C	Na+/K+ ATPase C-terminus	2.3e-145	496.3
509	Exonuclease	Exonuclease	1.3e-56	201.5
510	Glycos_trans f_1	Glycosyl transferases group 1	2.9e-06	27.0
511	Glycos_trans f_1	Glycosyl transferases group 1	2.9e-06	27.0
512	Glycos_trans f_1	Glycosyl transferases group 1	1.9e-09	38.5
514	pro_isomeras e	Cyclophilin type peptidyl-prolyl cis-tr	1.8e-63	221.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
515	EGF	EGF-like domain	1.9e-18	74.7
516	Surp	Surp module	4.3e-38	140.0
523	ig	Immunoglobulin domain	3.3e-06	25.0
526	UBX	UBX domain	1.1e-34	128.6
528	adh_zinc	Zinc-binding dehydrogenases	2.7e-34	127.4
530	SAM	SAM domain (Sterile alpha motif)	0.046	10.0
531	adh_short	short chain dehydrogenase	0.0025	-34.1
532	mito_carr	Mitochondrial carrier proteins	2.5e-81	281.7
533	mito_carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	FMO-like	Flavin-binding monooxygenase-like	0	1153.7
536	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
538	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
539	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	1.9e-117	403.6
540	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
541	vATP-synt_E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	zf-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
544	DUF101	Protein of unknown function DUF101	8.5e-38	139.0
545	TGFb_propept ide	TGF-beta propeptide	1.1e-67	238.2
547	WD40	WD domain, G-beta repeat	2.6e-32	120.8
548	RHD	Rel homology domain (RHD).	1.6e-238	686.2
549	MMR_HSR1	GTPase of unknown function	5.4e-67	236.0
551	HECT	HECT-domain (ubiquitin-transferase).	4.3e-127	435.6
554	MHC_II_alpha	Class II histocompatibility antigen, alp	3.5e-74	259.8
555	zf-UBR1	Putative zinc finger in N-recognin	3.3e-16	67.3
556	Kelch	Kelch motif	5.5e-29	109.7
561	AMP-binding	AMP-binding enzyme	2.8e-06	-163.7
562	PABP	Poly-adenylate binding protein, unique domai	4.9e-38	139.8
564	Gag_p30	Gag P30 core shell protein	1.2e-67	238.2
566	PWWP	PWWP domain	8.1e-16	66.0
567	SCAN	SCAN domain	7.3e-68	238.9
569	pkinase	Eukaryotic protein kinase domain	1.5e-84	294.3
570	pkinase	Eukaryotic protein kinase domain	1.5e-84	294.3
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin_head	Myosin head (motor domain)	0	1495.2
573	myosin_head	Myosin head (motor domain)	0	1490.4
575	Surp	Surp module	1.7e-23	91.5
576	Surp	Surp module	1.7e-23	91.5
577	DNA_pol_B	DNA polymerase family B	0	1138.6
578	PDZ	PDZ domain (Also known as DHR or GLGF).	8.3e-09	42.7
579	LRR	Leucine Rich Repeat	4.9e-21	83.3
580	neur_chan	Neurotransmitter-gated ion-channel	5.9e-177	601.3
583	sushi	Sushi domain (SCR repeat)	0	1673.0
584	DEAD	DEAD/DEAH box helicase	7.3e-36	116.3
586	KH-domain	KH domain	2.9e-13	57.5
587	G-patch	G-patch domain	2.3e-14	61.2
589	LIM	LIM domain containing proteins	2.3e-36	133.4
590	bromodomain	Bromodomain	6.6e-32	114.7
591	bromodomain	Bromodomain	6.6e-32	114.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
592	hormone_rec	Ligand-binding domain of nuclear hormone	3.5e-22	87.1
593	PHD	PHD-finger	3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase domain	5e-92	319.2
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_carr	Mitochondrial carrier proteins	6.3e-67	232.3
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PWWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_binding	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatase	Protein-tyrosine phosphatase	1.4e-32	121.6
622	pkinase	Eukaryotic protein kinase domain	4.4e-40	146.6
623	BNR	BNR repeat	2.1e-11	51.3
624	molybdopterin	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh_short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632	rrm	RNA recognition motif.	4e-05	30.5
635	pkinase	Eukaryotic protein kinase domain	1.6e-104	360.7
636	Fork_head	Fork head domain	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase domain	3.8e-70	246.5
642	TPR	TPR Domain	4.8e-08	40.1
643	efhand	EF hand	1.9e-27	104.6
647	SNF2_N	SNF2 and others N-terminal domain	1.2e-101	351.1
648	PseudoU_synth_2	RNA pseudouridylate synthase	1.9e-55	197.6
650	zf-C2H2	Zinc finger, C2H2 type	0.0087	22.7
651	ank	Ank repeat	1.3e-17	71.9
652	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
653	neur_chan	Neurotransmitter-gated ion-channel	4.1e-171	581.8
654	tsp_1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
661	pou	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
662	C2	C2 domain	6.7e-19	76.2
663	C2	C2 domain	6.7e-19	76.2
664	C2	C2 domain	6.7e-19	76.2
667	GST	Glutathione S-transferases.	9.3e-34	114.4
668	LRR	Leucine Rich Repeat	9.3e-31	115.6
670	spectrin	Spectrin repeat	4e-57	203.2
671	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
672	ABC_tran	ABC transporter	5.3e-60	212.8
674	WD40	WD domain, G-beta repeat	4.8e-24	93.3

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
675	WD40	WD domain, G-beta repeat	4.8e-24	93.3
676	LRR	Leucine Rich Repeat	0.0015	25.2
679	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-29	107.7
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
682	DSPc	Dual specificity phosphatase, catalytic doma	4.3e-43	156.6
683	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin	0	1890.8
689	PR55	Protein phosphatase 2A regulatory subunit PR	0	1038.8
691	homeobox	Homeobox domain	8.5e-30	112.4
696	Peptidase_M24	metallopeptidase family M24	2.6e-59	210.5
697	RhoGEF	RhoGEF domain	9.5e-35	128.9
698	PHD	PHD-finger	0.008	9.3
701	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
702	Sulfatase	Sulfatase	3e-231	781.6
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
707	Acyl_transf	Acyl transferase domain	1.1e-22	88.8
708	WD40	WD domain, G-beta repeat	4.8e-19	76.7
710	Ran_BP1	RanBP1 domain.	8.4e-06	-7.3
713	DEAD	DEAD/DEAH box helicase	9.9e-42	134.9
714	PH	PH domain	1.6e-09	39.0
715	DSPc	Dual specificity phosphatase, catalytic doma	1.5e-37	138.2
717	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
718	ig	Immunoglobulin domain	1e-29	100.8
719	integrin_B	Integrins, beta chain	0	1125.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	32.4
722	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
723	ig	Immunoglobulin domain	2.2e-05	22.4
724	F-box	F-box domain.	0.007	23.0
725	Nop	Putative snoRNA binding domain	8.1e-58	205.5
726	Nop	Putative snoRNA binding domain	8.1e-58	205.5
727	WD40	WD domain, G-beta repeat	7.5e-26	99.3
730	dsrm	Double-stranded RNA binding motif	0.027	12.1
731	dynamin	Dynamin family	4.2e-16	66.9
733	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.8e-10	41.7
735	CDP-OH_P_transf	CDP-alcohol phosphatidyltransferase	4.2e-26	100.1
738	DEAD	DEAD/DEAH box helicase	8.6e-57	182.5
739	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
742	ras	Ras family	2.2e-100	346.9
743	PMI_typeI	Phosphomannose isomerase type I	1.2e-243	822.9
747	trypsin	Trypsin	6.4e-88	279.4
748	kazal	Kazal-type serine protease inhibitor domain	2.2e-52	187.4
749	efhand	EF hand	6.3e-06	33.1
751	PHD	PHD-finger	4.9e-16	66.7
752	zf-C2H2	Zinc finger, C2H2 type	3.2e-21	83.9
753	Hydrolase	haloacid dehalogenase-like hydrolase	6.1e-11	49.8
754	Ribosomal_L39	Ribosomal L39 protein	0.00018	26.7
755	PH	PH domain	3.6e-14	55.7
758	SCAN	SCAN domain	1.4e-53	191.5
759	PA	PA domain	0.0065	23.1
760	arf	ADP-ribosylation factor family	2.2e-19	77.8
761	CIDE-N	CIDE-N domain	2.2e-40	147.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
762	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
763	zf-MYND	MYND finger	4.1e-14	60.3
764	pou	Pou domain - N-terminal to homeobox domain	1e-52	188.6
767	vwc	von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	EF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two domains)	2.4e-53	181.6
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	1e-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	G6PD	Glucose-6-phosphate dehydrogenase	1.5e-76	236.6
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito_carr	Mitochondrial carrier proteins	4.6e-57	198.5
782	SCAN	SCAN domain	1.3e-24	95.2
783	PDZ	PDZ domain (Also known as DHR or GLGF).	4.1e-07	37.1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase_HII	Ribonuclease HII	2.5e-67	237.1
790	PI3_PI4_kinase	Phosphatidylinositol 3- and 4-kinases	5.4e-108	372.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal-bind_lectin	Vertebrate galactoside-binding lectin	4.1e-25	88.7
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN_hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD_NFYB_HMF	Histone-like transcription factor	6e-14	59.8
812	adh_short	short chain dehydrogenase	8.1e-20	79.3
814	IMP4	Domain of unknown function	3.3e-71	250.0
815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
816	Pept_tRNA_hydro	Peptidyl-tRNA hydrolase	1.6e-37	138.0
817	ARID	ARID DNA binding domain	2.5e-18	74.3
826	IF5_eIF4_eIF2	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
830	ArfGap	Putative GTP-ase activating protein for Arf	1.5e-53	191.3
831	LRR	Leucine Rich Repeat	2.1e-26	101.1
832	laminin_EGF	Laminin EGF-like (Domains III and V)	2e-57	204.2
839	rrm	RNA recognition motif.	1.3e-22	88.5
840	Y_phosphatase	Protein-tyrosine phosphatase	2.6e-119	409.8
841	pkinase	Eukaryotic protein kinase domain	3.4e-100	346.3
844	Ribosomal_L22e	Ribosomal L22e protein family	1e-64	228.4
846	IBR	IBR domain	9e-15	62.5
849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.4e-07	26.5
850	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00016	18.9
851	SET	SET domain	5e-30	113.2
852	SRCR	Scavenger receptor cysteine-	0	1025.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
		rich domain		
853	SRCR	Scavenger receptor cysteine-rich domain	0	1025.4
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit VIa	3.4e-58	206.7
859	rrm	RNA recognition motif.	5.4e-45	162.9
861	PRK	Phosphoribulokinase	5.1e-62	219.4
863	mito_carr	Mitochondrial carrier proteins	2.9e-53	185.5
864	HSP90	Hsp90 protein	4.7e-158	538.5
866	ig	Immunoglobulin domain	4e-12	44.1
867	zf-C2H2	Zinc finger, C2H2 type	7e-135	461.5
872	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase_L_chain	Carbamoyl-phosphate synthase (CPSase)	2.1e-218	739.0
879	Ribosomal_S12e	Ribosomal protein S12e	2.1e-98	340.3
882	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	1.2e-51	182.0
884	RA	Ras association (RalGDS/AF-6) domain	0.044	8.0
887	DUF92	Integral membrane protein DUF92	2.7e-12	54.3
889	sugar_tr	Sugar (and other) transporter	8.2e-63	222.1
893	DUF28	Domain of unknown function DUF28	1.3e-43	158.3
896	IP_trans	Phosphatidylinositol transfer protein	6.5e-98	338.7
898	DEAD	DEAD/DEAH box helicase	1.5e-48	156.5
899	KE2	KE2 family protein	7e-61	215.7
900	KE2	KE2 family protein	4.3e-51	183.2
901	zf-C2H2	Zinc finger, C2H2 type	2.7e-57	203.8
902	ras	Ras family	2.3e-75	263.8
904	TPR	TPR Domain	3.2e-22	87.2
906	GBP	Guanylate-binding protein	8.9e-253	853.1
907	GBP	Guanylate-binding protein	1.1e-239	809.6
908	WD40	WD domain, G-beta repeat	2.6e-26	100.8
909	PH	PH domain	1.3e-09	39.4
910	zf-C2H2	Zinc finger, C2H2 type	2.5e-39	144.1
913	Epimerase	NAD dependent epimerase/dehydratase family	5e-07	-88.5
921	TBC	TBC domain	1.5e-09	30.7
922	WD40	WD domain, G-beta repeat	1.6e-25	98.2
923	WD40	WD domain, G-beta repeat	8.2e-07	36.1
924	Hydrolase	haloacid dehalogenase-like hydrolase	2.9e-05	29.1
925	UQ_con	Ubiquitin-conjugating enzyme	0.00033	-27.6
926	CH	Calponin homology (CH) domain	3.3e-53	190.2
928	WD40	WD domain, G-beta repeat	5.9e-48	172.7
929	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1e-10	37.4
930	Ribul_P_3_epim	Ribulose-phosphate 3 epimerase family	7.2e-105	361.8
931	Ribul_P_3_epim	Ribulose-phosphate 3 epimerase family	1.2e-96	334.4
936	C2	C2 domain	2.2e-62	220.7
937	NAP_family	Nucleosome assembly protein (NAP)	1.1e-22	84.6
940	abhydrolase	alpha/beta hydrolase fold	0.011	3.1
944	Tropomyosin	Tropomyosins	3.2e-07	25.1
948	pkinase	Eukaryotic protein kinase domain	3.4e-75	263.2
949	WD40	WD domain, G-beta repeat	1.8e-27	104.7
950	Acyltransferase	Acyltransferase	1.6e-07	38.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO_IDH_MocA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-OH_P_transf	CDP-alcohol phosphatidyltransferase	0.053	-22.2
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh_short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969	IF-2B	Initiation factor 2 subunit family	8.4e-193	653.9
970	RNase_PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L17	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestrin	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase, 20 Kd sub	4.8e-63	222.9
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_endo	tRNA intron endonuclease	0.0017	-34.2
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.012	11.6
1000	mito_carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6) domain	1.2e-15	65.4
1004	DUF81	Domain of unknown function DUF81	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family	3.7e-195	661.8
1008	TPR	TPR Domain	8.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.7e-15	53.1
1016	tRNA-synt_2c	tRNA synthetases class II (A)	2.3e-15	55.2
1018	RhoGAP	RhoGAP domain	1.6e-78	274.3
1022	PGAM	Phosphoglycerate mutase family	3.8e-18	69.7
1026	HMG_box	HMG (high mobility group) box	8.4e-20	79.2
1027	TBC	TBC domain	7.3e-45	162.5
1028	UQ_con	Ubiquitin-conjugating enzyme	1.4e-49	178.1
1032	PDZ	PDZ domain (Also known as DHR or GLGF).	0.028	16.3
1034	Hydrolase	haloacid dehalogenase-like hydrolase	2e-21	84.6
1037	KRAB	KRAB box	4.8e-06	32.4
1038	Cation_efflux	Cation efflux family	7.1e-42	152.5
1040	ART	NAD:arginine ADP-ribosyltransferase	4.7e-47	169.1
1042	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1043	zf-C2H2	Zinc finger, C2H2 type	3.7e-24	93.7
1045	lectin_c	Lectin C-type domain	1.9e-28	108.0
1046	Glucosamine_iso	Glucosamine-6-phosphate isomerase	0.00013	-25.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	ig	Immunoglobulin domain	1.7e-09	35.6
1050	Ribosomal_L24e	Ribosomal protein L24e	2e-33	124.5
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-44	159.2
1059	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1060	homeobox	Homeobox domain	3.2e-31	117.2
1062	Acyltransferase	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1_OBG	GTP1/OBG family	4.8e-41	141.8
1071	ig	Immunoglobulin domain	8.4e-48	159.1
1072	PHD	PHD-finger	6.8e-07	36.3
1074	DENN	DENN (AEX-3) domain	8.3e-33	121.5
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1077	OLF	Olfactomedin-like domain	2.2e-66	234.0
1078	mito_carr	Mitochondrial carrier proteins	1e-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSPc	Dual specificity phosphatase, catalytic doma	3.3e-63	223.4
1094	GSHPx	Glutathione peroxidases	9.6e-41	148.8
1095	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	DUF25	Domain of unknown function DUF25	6e-75	262.4
1105	Nitroreductase	Nitroreductase family	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1.3e-179	610.1
1107	DAGKc	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7
1116	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14_17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolase	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase domain	1.4e-94	327.6
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
1129	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	2.2e-56	197.1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
1136	Adap_comp_sub	Adaptor complexes medium subunit family	1.2e-256	866.0
1137	Adap_comp_sub	Adaptor complexes medium subunit family	2.5e-209	708.8
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransferase	Acyltransferase	1.2e-05	29.9
1153	IRS	PTB domain (IRS-1 type)	5.4e-55	196.1
1155	ig	Immunoglobulin domain	1.3e-31	106.9
1157	Asparaginase_2	Asparaginase	6.4e-72	252.3
1159	GMC_oxred	GMC oxidoreductases	4.7e-142	485.3
1160	zf-AN1	AN1-like Zinc finger	0.00021	27.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1163	linker_histone	linker histone H1 and H5 family	3.8e-14	60.4
1164	DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	SAM domain (Sterile alpha motif)	0.04	10.5
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1_MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGEF domain	1.7e-88	307.4
1185	mito_carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR_LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn_DAP_Arg_deC	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Sec1	Sec1 family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf_8	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh_short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie_methyltran	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm_3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP-synt_AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	rrm	RNA recognition motif.	2.1e-40	147.7
1220	DUF6	Integral membrane protein DUF6	0.015	21.5
1222	SCAN	SCAN domain	1.5e-71	251.1
1223	G-gamma	GGL domain	3.6e-36	129.5
1227	catalase	Catalase	0	1158.9
1232	PX	PX domain	2.2e-15	64.5
1233	PX	PX domain	2.2e-15	64.5
1236	FCH	Fes/CIP4 homology domain	3.3e-09	44.0
1241	Peptidase_M20	Peptidase family M20/M25/M40	2e-63	224.1
1243	WW	WW domain	0.044	17.9
1247	UPF0006	Metalloenzyme of unknown function UPF0006	6.3e-61	215.8
1248	Glycos_transf_2	Glycosyl transferases	4.5e-10	46.9
1249	efhand	EF hand	4e-11	50.4
1254	UQ_con	Ubiquitin-conjugating enzyme	2.1e-73	257.3
1255	ras	Ras family	2.2e-62	220.7
1256	formyl_transf	Formyl transferase	4.9e-30	108.3
1259	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-13	46.4
1261	DiHfolate_red	Dihydrofolate reductase	2.1e-69	241.7
1262	G_glu_transpept	Gamma-glutamyltranspeptidase	1.8e-110	380.4
1263	PAS	PAS domain	1.3e-08	36.9
1265	LRR	Leucine Rich Repeat	4.2e-22	86.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1266	SCP	SCP-like extracellular protein	6e-29	108.0
1267	K_tetra	K+ channel tetramerisation domain	2.8e-27	104.0
1269	ras	Ras family	1.3e-85	297.9
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine-binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1298	LIM	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1307	mito_carr	Mitochondrial carrier proteins	2.1e-53	186.0
1308	WD40	WD domain, G-beta repeat	1.6e-17	71.6
1310	UPAR_LY6	u-PAR/Ly-6 domain	7.1e-20	75.5
1313	thiored	Thioredoxin	3.6e-05	21.6
1314	Aa_trans	Transmembrane amino acid transporter protein	1.5e-67	237.9
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L13	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_seg	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_synthetase	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
1335	UPP_synthetase	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPc	Dual specificity phosphatase, catalytic doma	1.2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band_41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1347	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomera	0.086	-177.2
1348	BTB	BTB/POZ domain	5.3e-28	106.5
1349	DUF6	Integral membrane protein DUF6	0.033	15.8
1350	myosin_head	Myosin head (motor domain)	0	1088.7
1352	Nramp	Natural resistance-associated macrophage pro	1.2e-202	686.6
1353	S_100	S-100/ICaBP type calcium binding domain	5.3e-23	89.9
1355	DEAD	DEAD/DEAH box helicase	3.6e-65	209.0
1356	C2	C2 domain	2.4e-15	64.4
1357	RBD	Raf-like Ras-binding domain	4.2e-57	203.1
1360	zf-C2H2	Zinc finger, C2H2 type	7.4e-141	481.4
1361	HMG14_17	HMG14 and HMG17	7.9e-40	145.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1362	SIS	SIS domain	3.8e-30	113.6
1363	SIS	SIS domain	1.3e-28	108.5
1364	ig	Immunoglobulin domain	0.00026	19.0
1368	K_tetra	K+ channel tetramerisation domain	1.1e-16	68.9
1371	Collagen	Collagen triple helix repeat (20 copies)	2.2e-113	390.1
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	ELM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	BTB	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-09	35.6
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	kinesin	Kinesin motor domain	7.8e-188	637.4
1394	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1398	KRAB	KRAB box	5.1e-22	86.6
1402	bZIP	bZIP transcription factor	0.035	13.1
1405	sugar_tr	Sugar (and other) transporter	0.003	-101.5
1406	RhoGAP	RhoGAP domain	8.9e-47	168.8
1407	rrm	RNA recognition motif.	1e-35	132.1
1408	LRR	Leucine Rich Repeat	2.1e-13	58.0
1409	Nebulin_repeat	Nebulin repeat	6e-54	192.6
1410	ank	Ank repeat	1.6e-17	71.6
1412	Ribosomal_L5_C	ribosomal L5P family C-terminus	8.2e-58	205.5
1415	trypsin	Trypsin	4.7e-85	270.4
1416	aminotran_1	Aminotransferases class-I	4.4e-05	-91.2
1417	S1	S1 RNA binding domain	1.6e-07	33.1
1419	WD40	WD domain, G-beta repeat	2.2e-09	44.6
1422	cadherin	Cadherin domain	8.3e-42	152.3
1424	SH3	SH3 domain	2.5e-80	280.3
1425	PHD	PHD-finger	3.2e-17	70.6
1426	PHD	PHD-finger	3.2e-17	70.6
1427	ArfGap	Putative GTP-ase activating protein for Arf	1e-37	138.8
1428	helicase_C	Helicases conserved C-terminal domain	1e-26	102.2
1429	WD40	WD domain, G-beta repeat	3.9e-07	37.2
1430	inositol_P	Inositol monophosphatase family	2.5e-10	40.2
1431	mito_carr	Mitochondrial carrier proteins	4.3e-83	287.7
1433	C1q	C1q domain	2.9e-16	66.2
1434	WD40	WD domain, G-beta repeat	1.6e-13	58.3
1435	Inos-1-P_synth	Myo-inositol-1-phosphate synthase	7e-228	770.4
1436	rrm	RNA recognition motif.	1.4e-34	128.3
1438	ig	Immunoglobulin domain	1.3e-12	45.6
1440	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1441	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1443	Kelch	Kelch motif	0.00013	28.7
1446	ARID	ARID DNA binding domain	1.8e-21	84.7
1447	zf-C2H2	Zinc finger, C2H2 type	9.4e-28	105.6
1448	AMP-binding	AMP-binding enzyme	2.6e-07	-145.1
1451	rrm	RNA recognition motif.	6.5e-21	82.9
1454	ig	Immunoglobulin domain	5.6e-44	146.7
1455	Sialyltransf	Sialyltransferase family	5.4e-21	83.2
1460	Aldose_epim	Aldose 1-epimerase	1.9e-35	131.2
1461	C2	C2 domain	4e-18	73.6
1470	TIG	IPT/TIG domain	3.1e-19	77.3
1472	PseudoU_synt	RNA pseudouridylate synthase	4.3e-16	66.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	h_2			
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
1475	Cation_efflux	Cation efflux family	4.6e-49	176.4
1477	TBC	TBC domain	8e-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480	ig	Immunoglobulin domain	5.5e-06	24.3
1484	Telo_bind_alpha	Telomere-binding protein alpha subuni	0.028	-225.9
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1486	pkinase	Eukaryotic protein kinase domain	9.5e-13	49.9
1488	helicase_C	Helicases conserved C-terminal domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase family	5.2e-41	149.7
1491	guanylate_cyc	Adenylate and Guanylate cyclase catalyt	5.9e-46	166.1
1492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.1e-10	36.3
1497	pkinase	Eukaryotic protein kinase domain	1e-22	85.8
1500	SH3	SH3 domain	9.3e-05	27.2
1502	homeobox	Homeobox domain	0.084	13.8
1503	homeobox	Homeobox domain	0.084	13.8
1505	EGF	EGF-like domain	2.7e-23	90.8
1506	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.7e-21	84.2
1508	Peptidase_M20	Peptidase family M20/M25/M40	2.8e-28	101.8
1511	PX	PX domain	1.9e-11	51.5
1512	Sulfatase	Sulfatase	2.8e-35	130.7
1516	Syntaxin	Syntaxin	0.011	-62.3
1518	aminotran_3	Aminotransferases class-III pyridoxal-pho	9.7e-106	305.6
1520	ig	Immunoglobulin domain	0.075	11.0
1521	RA	Ras association (RalGDS/AF-6) domain	0.013	13.3
1523	RhoGAP	RhoGAP domain	2.5e-05	18.7
1528	WD40	WD domain, G-beta repeat	5.4e-24	93.1
1535	IMS	impB/mucB/samB family	7.8e-95	328.5
1538	FYVE	FYVE zinc finger	3.2e-27	101.5
1539	DAGKc	Diacylglycerol kinase catalytic domain	6e-07	36.5
1540	Ocular_alb	Ocular albinism type 1 protein	0	1184.7
1653	SAP	SAP domain	6e-06	33.2
1654	Amino_oxidase	Flavin containing amine oxidase	3.2e-43	157.0
1655	Amino_oxidase	Flavin containing amine oxidase	3.2e-43	157.0
1656	RhoGEF	RhoGEF domain	1.4e-24	95.1
1657	MMR_HSR1	GTPase of unknown function	0.0011	-45.5
1659	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.5e-11	51.1
1660	actin	Actin	6.6e-21	69.9
1661	BAH	BAH domain	1.7e-82	287.5
1662	vwa	von Willebrand factor type A domain	0	1909.4
1663	WD40	WD domain, G-beta repeat	1.4e-67	237.9
1667	zf-C2H2	Zinc finger, C2H2 type	1.3e-93	324.4
1669	Nol1_Nop2_Sun	NOL1/NOP2/sun family	1.3e-23	84.3
1671	SH2	Src homology domain 2	5.4e-15	46.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1672	chromo	'chromo' (CHRromatin Organization MOdifier)	2.1e-18	67.7
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	0.0025	17.6
1676	Glyco_hydro_47	Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_47	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1681	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1683	MMR_HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduct	Ferric reductase like transmembrane com	8.4e-82	285.2
1698	Ferric_reduct	Ferric reductase like transmembrane com	3.5e-53	190.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP_EFTU	Elongation factor Tu family	0.014	11.4
1703	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG_box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	dsrm	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine dimethylases	0.045	9.2
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacetyl	Histone deacetylase family	1.7e-104	360.6
1735	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.0023	16.1
1743	ras	Ras family	3.7e-10	-21.3
1744	ras	Ras family	3.7e-10	-21.3
1745	RasGEF	RasGEF domain	3.2e-49	176.9
1746	adh_short	short chain dehydrogenase	7.1e-08	34.6
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	142.2
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758	rrm	RNA recognition motif.	0.017	21.2
1760	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1761	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1765	MMR_HSR1	GTPase of unknown function	6.4e-41	149.4
1769	CN_hydrolase	Carbon-nitrogen hydrolase	3e-06	-43.9
1775	ank	Ank repeat	4.1e-07	37.1
1779	Oxysterol_BP	Oxysterol-binding protein	4.7e-56	199.6
1783	RhoGEF	RhoGEF domain	1.6e-23	91.6
1784	RhoGEF	RhoGEF domain	1.6e-23	91.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN01!.DOC)

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1	1-21	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.982	0.901
10	1-21	0.991	0.955
11	1-23	0.989	0.899
12	1-25	0.955	0.803
13	1-18	0.932	0.625
14	1-18	0.938	0.876
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.953	0.840
20	1-20	0.935	0.701
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	0.976
32	1-22	0.998	0.909
35	1-33	0.949	0.736
36	1-33	0.949	0.736
46	1-19	0.970	0.951
67	1-25	0.968	0.848
71	1-18	0.949	0.845
72	1-30	0.991	0.919
75	1-29	0.958	0.854
88	1-20	0.986	0.945
94	1-33	0.994	0.943
97	1-46	0.964	0.595
103	1-49	0.983	0.570
108	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
162	1-25	0.937	0.729
168	1-16	0.939	0.826
171	1-27	0.964	0.777
178	1-21	0.945	0.825
180	1-27	0.981	0.941
187	1-28	0.982	0.936
190	1-19	0.953	0.840
196	1-22	0.975	0.916
197	1-22	0.963	0.936

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211	1-28	0.971	0.849
216	1-24	0.986	0.956
218	1-33	0.961	0.895
219	1-19	0.970	0.871
221	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.955
245	1-30	0.970	0.722
248	1-22	0.976	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
272	1-24	0.953	0.739
283	1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302	1-28	0.980	0.893
304	1-16	0.907	0.635
312	1-19	0.993	0.976
313	1-17	0.930	0.753
323	1-22	0.998	0.909
324	1-17	0.982	0.954
328	1-19	0.971	0.865
329	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.920	0.712
332	1-24	0.975	0.881
333	1-19	0.984	0.941
334	1-20	0.899	0.567
335	1-27	0.942	0.813
336	1-20	0.952	0.850
337	1-38	0.942	0.653
338	1-27	0.973	0.772
339	1-36	0.979	0.804
340	1-27	0.888	0.597
343	1-19	0.971	0.865
344	1-22	0.994	0.928
345	1-17	0.966	0.687
346	1-19	0.936	0.822
347	1-22	0.963	0.924
349	1-24	0.982	0.966
351	1-21	0.918	0.815
352	1-31	0.988	0.912
354	1-31	0.974	0.839
355	1-29	0.932	0.632
356	1-15	0.994	0.969
357	1-33	0.935	0.726
360	1-27	0.938	0.827
361	1-25	0.954	0.674
362	1-22	0.929	0.788
363	1-21	0.881	0.715
364	1-33	0.978	0.841
365	1-33	0.978	0.841

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370	1-24	0.920	0.712
371	1-24	0.961	0.773
372	1-27	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-26	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	0.962
411	1-38	0.977	0.827
412	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	0.940
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-22	0.889	0.785
422	1-48	0.982	0.862
424	1-19	0.979	0.933
428	1-38	0.942	0.653
430	1-18	0.947	0.595
432	1-33	0.957	0.789
433	1-26	0.979	0.904
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
443	1-15	0.966	0.940
448	1-36	0.979	0.804
453	1-41	0.958	0.609
455	1-33	0.943	0.606
457	1-27	0.888	0.597
462	1-16	0.925	0.681
486	1-27	0.972	0.845
495	1-24	0.917	0.636
498	1-26	0.993	0.890
505	1-20	0.976	0.926
507	1-17	0.966	0.687
510	1-23	0.930	0.593

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	0.966
550	1-30	0.933	0.713
552	1-21	0.973	0.912
554	1-23	0.969	0.784
571	1-21	0.918	0.815
574	1-31	0.988	0.912
580	1-39	0.925	0.556
594	1-31	0.974	0.839
608	1-29	0.932	0.632
609	1-29	0.932	0.632
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.935	0.726
653	1-27	0.938	0.827
668	1-22	0.929	0.788
677	1-16	0.948	0.807
685	1-21	0.881	0.715
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.860	0.562
713	1-25	0.966	0.743
718	1-19	0.936	0.822
719	1-20	0.961	0.824
729	1-29	0.972	0.874
735	1-46	0.903	0.598
746	1-14	0.916	0.730
747	1-22	0.965	0.876
748	1-29	0.968	0.785
759	1-24	0.961	0.773
767	1-27	0.919	0.768
768	1-33	0.900	0.585
773	1-42	0.959	0.702
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820	1-17	0.995	0.950
827	1-49	0.971	0.749
848	1-20	0.968	0.874
864	1-20	0.928	0.782
866	1-19	0.986	0.934
873	1-23	0.948	0.886
881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
950	1-29	0.957	0.845
963	1-20	0.981	0.900
964	1-20	0.886	0.558
973	1-16	0.968	0.890
980	1-34	0.961	0.749
981	1-20	0.953	0.822
984	1-12	0.938	0.780
1015	1-22	0.985	0.854
1040	1-46	0.977	0.698
1052	1-18	0.969	0.842
1059	1-20	0.927	0.867
1065	1-33	0.983	0.918
1069	1-22	0.993	0.935

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1075	1-27	0.992	0.934
1080	1-19	0.931	0.829
1092	1-19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-38	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
1189	1-35	0.967	0.839
1192	1-46	0.993	0.638
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	0.789
1380	1-26	0.979	0.904
1397	1-27	0.962	0.777
1399	1-23	0.997	0.960
1404	1-24	0.998	0.977
1410	1-15	0.946	0.845
1414	1-24	0.913	0.588
1415	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.967	0.899
1430	1-34	0.977	0.819
1431	1-28	0.979	0.923
1432	1-36	0.957	0.613
1433	1-32	0.921	0.753
1434	1-39	0.983	0.621
1435	1-25	0.910	0.631
1436	1-42	0.988	0.868
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	0.891
1561	1-25	0.967	0.899
1580	1-17	0.923	0.824
1593	1-28	0.979	0.923

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TABLE 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1	1787	3573	5359	784CIP2_1	1103
2	1788	3574	5360	784CIP2_2	2673
3	1789	3575	5361	784CIP2_3	4117
4	1790	3576	5362	784CIP2_4	5556
5	1791	3577	5363	784CIP2_5	5562
6	1792	3578	5364	784CIP2_6	5562
7	1793	3579	5365	784CIP2_7	5562
8	1794	3580	5366	784CIP2_8	5562
9	1795	3581	5367	784CIP2_9	5563
10	1796	3582	5368	784CIP2_10	5564
11	1797	3583	5369	784CIP2_11	5565
12	1798	3584	5370	784CIP2_12	5689
13	1799	3585	5371	784CIP2_13	5729
14	1800	3586	5372	784CIP2_14	5745
15	1801	3587	5373	784CIP2_15	5777
16	1802	3588	5374	784CIP2_16	5777
17	1803	3589	5375	784CIP2_17	5789
18	1804	3590	5376	784CIP2_18	5792
19	1805	3591	5377	784CIP2_19	5804
20	1806	3592	5378	784CIP2_20	5805
21	1807	3593	5379	784CIP2_21	5805
22	1808	3594	5380	784CIP2_22	5844
23	1809	3595	5381	784CIP2_23	5844
24	1810	3596	5382	784CIP2_24	5850
25	1811	3597	5383	784CIP2_25	5867
26	1812	3598	5384	784CIP2_26	5973
27	1813	3599	5385	784CIP2_27	5995
28	1814	3600	5386	784CIP2_28	5995
29	1815	3601	5387	784CIP2_29	6005
30	1816	3602	5388	784CIP2_30	6007
31	1817	3603	5389	784CIP2_31	6007
32	1818	3604	5390	784CIP2_32	6009
33	1819	3605	5391	784CIP2_33	6012
34	1820	3606	5392	784CIP2_34	6015
35	1821	3607	5393	784CIP2_35	6016
36	1822	3608	5394	784CIP2_36	6016
37	1823	3609	5395	784CIP2_37	6018
38	1824	3610	5396	784CIP2_38	6018
39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828	3614	5400	784CIP2_42	6081
43	1829	3615	5401	784CIP2_43	6089
44	1830	3616	5402	784CIP2_44	6118
45	1831	3617	5403	784CIP2_45	6118
46	1832	3618	5404	784CIP2_46	6130
47	1833	3619	5405	784CIP2_47	6177
48	1834	3620	5406	784CIP2_48	6189
49	1835	3621	5407	784CIP2_49	6191
50	1836	3622	5408	784CIP2_50	6204
51	1837	3623	5409	784CIP2_51	6204
52	1838	3624	5410	784CIP2_52	6284
53	1839	3625	5411	784CIP2_53	6367
54	1840	3626	5412	784CIP2_54	6436
55	1841	3627	5413	784CIP2_55	6442
56	1842	3628	5414	784CIP2_56	6445
57	1843	3629	5415	784CIP2_57	6457
58	1844	3630	5416	784CIP2_58	6458
59	1845	3631	5417	784CIP2_59	6458

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
60	1846	3632	5418	784CIP2_60	6462
61	1847	3633	5419	784CIP2_61	6472
62	1848	3634	5420	784CIP2_62	6499
63	1849	3635	5421	784CIP2_63	6499
64	1850	3636	5422	784CIP2_64	6505
65	1851	3637	5423	784CIP2_65	6534
66	1852	3638	5424	784CIP2_66	6534
67	1853	3639	5425	784CIP2_67	6540
68	1854	3640	5426	784CIP2_68	6550
69	1855	3641	5427	784CIP2_69	6550
70	1856	3642	5428	784CIP2_70	6592
71	1857	3643	5429	784CIP2_71	6645
72	1858	3644	5430	784CIP2_72	6671
73	1859	3645	5431	784CIP2_73	6763
74	1860	3646	5432	784CIP2_74	6763
75	1861	3647	5433	784CIP2_75	6786
76	1862	3648	5434	784CIP2_76	6824
77	1863	3649	5435	784CIP2_77	6830
78	1864	3650	5436	784CIP2_78	6831
79	1865	3651	5437	784CIP2_79	6832
80	1866	3652	5438	784CIP2_80	6834
81	1867	3653	5439	784CIP2_81	6834
82	1868	3654	5440	784CIP2_82	6835
83	1869	3655	5441	784CIP2_83	6837
84	1870	3656	5442	784CIP2_84	6843
85	1871	3657	5443	784CIP2_85	6859
86	1872	3658	5444	784CIP2_86	6915
87	1873	3659	5445	784CIP2_87	6932
88	1874	3660	5446	784CIP2_88	6957
89	1875	3661	5447	784CIP2_89	6961
90	1876	3662	5448	784CIP2_90	6973
91	1877	3663	5449	784CIP2_91	6973
92	1878	3664	5450	784CIP2_93	7007
93	1879	3665	5451	784CIP2_94	7018
94	1880	3666	5452	784CIP2_95	7019
95	1881	3667	5453	784CIP2_96	7020
96	1882	3668	5454	784CIP2_97	7020
97	1883	3669	5455	784CIP2_98	7021
98	1884	3670	5456	784CIP2_99	7023
99	1885	3671	5457	784CIP2_100	7027
100	1886	3672	5458	784CIP2_101	7028
101	1887	3673	5459	784CIP2_102	7029
102	1888	3674	5460	784CIP2_103	7031
103	1889	3675	5461	784CIP2_104	7032
104	1890	3676	5462	784CIP2_105	7033
105	1891	3677	5463	784CIP2_106	7035
106	1892	3678	5464	784CIP2_107	7036
107	1893	3679	5465	784CIP2_108	7039
108	1894	3680	5466	784CIP2_109	7043
109	1895	3681	5467	784CIP2_110	7044
110	1896	3682	5468	784CIP2_111	7046
111	1897	3683	5469	784CIP2_112	7054
112	1898	3684	5470	784CIP2_113	7061
113	1899	3685	5471	784CIP2_114	7077
114	1900	3686	5472	784CIP2_115	7092
115	1901	3687	5473	784CIP2_116	7094
116	1902	3688	5474	784CIP2_117	7106
117	1903	3689	5475	784CIP2_118	7107
118	1904	3690	5476	784CIP2_119	7111
119	1905	3691	5477	784CIP2_120	7123
120	1906	3692	5478	784CIP2_121	7142
121	1907	3693	5479	784CIP2_122	7142

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
122	1908	3694	5480	784CIP2_123	7154
123	1909	3695	5481	784CIP2_124	7160
124	1910	3696	5482	784CIP2_125	7169
125	1911	3697	5483	784CIP2_126	7185
126	1912	3698	5484	784CIP2_127	7197
127	1913	3699	5485	784CIP2_128	7219
128	1914	3700	5486	784CIP2_129	7226
129	1915	3701	5487	784CIP2_130	7229
130	1916	3702	5488	784CIP2_131	7234
131	1917	3703	5489	784CIP2_132	7235
132	1918	3704	5490	784CIP2_133	7235
133	1919	3705	5491	784CIP2_134	7238
134	1920	3706	5492	784CIP2_135	7247
135	1921	3707	5493	784CIP2_136	7261
136	1922	3708	5494	784CIP2_137	7262
137	1923	3709	5495	784CIP2_138	7267
138	1924	3710	5496	784CIP2_139	7272
139	1925	3711	5497	784CIP2_140	7273
140	1926	3712	5498	784CIP2_141	7282
141	1927	3713	5499	784CIP2_142	7288
142	1928	3714	5500	784CIP2_143	7291
143	1929	3715	5501	784CIP2_144	7293
144	1930	3716	5502	784CIP2_145	7294
145	1931	3717	5503	784CIP2_146	7299
146	1932	3718	5504	784CIP2_147	7300
147	1933	3719	5505	784CIP2_148	7312
148	1934	3720	5506	784CIP2_149	7313
149	1935	3721	5507	784CIP2_150	7315
150	1936	3722	5508	784CIP2_151	7318
151	1937	3723	5509	784CIP2_152	7321
152	1938	3724	5510	784CIP2_153	7330
153	1939	3725	5511	784CIP2_154	7331
154	1940	3726	5512	784CIP2_155	7333
155	1941	3727	5513	784CIP2_156	7350
156	1942	3728	5514	784CIP2_157	7352
157	1943	3729	5515	784CIP2_158	7384
158	1944	3730	5516	784CIP2_159	7403
159	1945	3731	5517	784CIP2_160	7431
160	1946	3732	5518	784CIP2_161	7441
161	1947	3733	5519	784CIP2_162	7453
162	1948	3734	5520	784CIP2_163	7467
163	1949	3735	5521	784CIP2_164	7471
164	1950	3736	5522	784CIP2_165	7493
165	1951	3737	5523	784CIP2_166	7502
166	1952	3738	5524	784CIP2_167	7511
167	1953	3739	5525	784CIP2_168	7514
168	1954	3740	5526	784CIP2_169	7520
169	1955	3741	5527	784CIP2_170	7541
170	1956	3742	5528	784CIP2_171	7570
171	1957	3743	5529	784CIP2_172	7578
172	1958	3744	5530	784CIP2_173	7583
173	1959	3745	5531	784CIP2_174	7592
174	1960	3746	5532	784CIP2_175	7601
175	1961	3747	5533	784CIP2_176	7602
176	1962	3748	5534	784CIP2_177	7608
177	1963	3749	5535	784CIP2_178	7615
178	1964	3750	5536	784CIP2_179	7617
179	1965	3751	5537	784CIP2_181	7624
180	1966	3752	5538	784CIP2_182	7626
181	1967	3753	5539	784CIP2_183	7640
182	1968	3754	5540	784CIP2_184	7641
183	1969	3755	5541	784CIP2_185	7641

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
184	1970	3756	5542	784CIP2_186	7641
185	1971	3757	5543	784CIP2_187	7642
186	1972	3758	5544	784CIP2_188	7649
187	1973	3759	5545	784CIP2_189	7656
188	1974	3760	5546	784CIP2_190	7657
189	1975	3761	5547	784CIP2_191	7657
190	1976	3762	5548	784CIP2_192	7662
191	1977	3763	5549	784CIP2_193	7668
192	1978	3764	5550	784CIP2_194	7673
193	1979	3765	5551	784CIP2_195	7690
194	1980	3766	5552	784CIP2_196	7700
195	1981	3767	5553	784CIP2_197	7709
196	1982	3768	5554	784CIP2_198	7736
197	1983	3769	5555	784CIP2_199	7737
198	1984	3770	5556	784CIP2_200	7744
199	1985	3771	5557	784CIP2_201	7771
200	1986	3772	5558	784CIP2_202	7786
201	1987	3773	5559	784CIP2_203	7791
202	1988	3774	5560	784CIP2_204	7797
203	1989	3775	5561	784CIP2_205	7806
204	1990	3776	5562	784CIP2_206	7812
205	1991	3777	5563	784CIP2_207	7812
206	1992	3778	5564	784CIP2_208	7818
207	1993	3779	5565	784CIP2_209	7822
208	1994	3780	5566	784CIP2_210	7827
209	1995	3781	5567	784CIP2_211	7830
210	1996	3782	5568	784CIP2_212	7835
211	1997	3783	5569	784CIP2_214	7840
212	1998	3784	5570	784CIP2_215	7858
213	1999	3785	5571	784CIP2_216	7858
214	2000	3786	5572	784CIP2_217	7861
215	2001	3787	5573	784CIP2_218	7866
216	2002	3788	5574	784CIP2_219	7868
217	2003	3789	5575	784CIP2_220	7896
218	2004	3790	5576	784CIP2_221	7898
219	2005	3791	5577	784CIP2_222	7900
220	2006	3792	5578	784CIP2_223	7906
221	2007	3793	5579	784CIP2_224	7908
222	2008	3794	5580	784CIP2_225	7909
223	2009	3795	5581	784CIP2_226	7917
224	2010	3796	5582	784CIP2_227	7932
225	2011	3797	5583	784CIP2_228	7940
226	2012	3798	5584	784CIP2_229	7940
227	2013	3799	5585	784CIP2_230	7984
228	2014	3800	5586	784CIP2_231	7984
229	2015	3801	5587	784CIP2_232	8001
230	2016	3802	5588	784CIP2_233	8021
231	2017	3803	5589	784CIP2_234	8029
232	2018	3804	5590	784CIP2_235	8033
233	2019	3805	5591	784CIP2_236	8040
234	2020	3806	5592	784CIP2_237	8052
235	2021	3807	5593	784CIP2_238	8096
236	2022	3808	5594	784CIP2_239	8096
237	2023	3809	5595	784CIP2_240	8113
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2_242	8132
240	2026	3812	5598	784CIP2_243	8137
241	2027	3813	5599	784CIP2_244	8137
242	2028	3814	5600	784CIP2_245	8159
243	2029	3815	5601	784CIP2_246	8159
244	2030	3816	5602	784CIP2_247	8161
245	2031	3817	5603	784CIP2_248	8176

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
246	2032	3818	5604	784CIP2_249	8196
247	2033	3819	5605	784CIP2_250	8200
248	2034	3820	5606	784CIP2_251	8212
249	2035	3821	5607	784CIP2_252	8220
250	2036	3822	5608	784CIP2_253	8238
251	2037	3823	5609	784CIP2_254	8254
252	2038	3824	5610	784CIP2_255	8255
253	2039	3825	5611	784CIP2_256	8288
254	2040	3826	5612	784CIP2_257	8296
255	2041	3827	5613	784CIP2_258	8329
256	2042	3828	5614	784CIP2_259	8362
257	2043	3829	5615	784CIP2_260	8429
258	2044	3830	5616	784CIP2_261	8436
259	2045	3831	5617	784CIP2_262	8448
260	2046	3832	5618	784CIP2_263	8472
261	2047	3833	5619	784CIP2_264	8502
262	2048	3834	5620	784CIP2_265	8504
263	2049	3835	5621	784CIP2_266	8507
264	2050	3836	5622	784CIP2_268	8509
265	2051	3837	5623	784CIP2_269	8515
266	2052	3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268	2054	3840	5626	784CIP2_272	8532
269	2055	3841	5627	784CIP2_273	8532
270	2056	3842	5628	784CIP2_274	8539
271	2057	3843	5629	784CIP2_275	8541
272	2058	3844	5630	784CIP2_276	8543
273	2059	3845	5631	784CIP2_277	8593
274	2060	3846	5632	784CIP2_278	8595
275	2061	3847	5633	784CIP2_279	8615
276	2062	3848	5634	784CIP2_280	8620
277	2063	3849	5635	784CIP2_281	8621
278	2064	3850	5636	784CIP2_282	8623
279	2065	3851	5637	784CIP2_283	8625
280	2066	3852	5638	784CIP2_284	8628
281	2067	3853	5639	784CIP2_285	8628
282	2068	3854	5640	784CIP2_286	8629
283	2069	3855	5641	784CIP2_287	8630
284	2070	3856	5642	784CIP2_288	8631
285	2071	3857	5643	784CIP2_289	8633
286	2072	3858	5644	784CIP2_290	8634
287	2073	3859	5645	784CIP2_291	8635
288	2074	3860	5646	784CIP2_292	8636
289	2075	3861	5647	784CIP2_293	8659
290	2076	3862	5648	784CIP2_294	8660
291	2077	3863	5649	784CIP2_295	8667
292	2078	3864	5650	784CIP2_296	8667
293	2079	3865	5651	784CIP2_297	8685
294	2080	3866	5652	784CIP2_298	8805
295	2081	3867	5653	784CIP2_299	8896
296	2082	3868	5654	784CIP2_300	8978
297	2083	3869	5655	784CIP2_301	9046
298	2084	3870	5656	784CIP2_302	9048
299	2085	3871	5657	784CIP2_303	9116
300	2086	3872	5658	784CIP2_304	9195
301	2087	3873	5659	784CIP2_305	9201
302	2088	3874	5660	784CIP2_306	9307
303	2089	3875	5661	784CIP2_307	9321
304	2090	3876	5662	784CIP2_308	9397
305	2091	3877	5663	784CIP2_309	9405
306	2092	3878	5664	784CIP2_310	9406
307	2093	3879	5665	784CIP2_311	9422

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
308	2094	3880	5666	784CIP2_312	9494
309	2095	3881	5667	784CIP2_313	9512
310	2096	3882	5668	784CIP2_314	9632
311	2097	3883	5669	784CIP2_315	9661
312	2098	3884	5670	784CIP2_316	9664
313	2099	3885	5671	784CIP2_317	9691
314	2100	3886	5672	784CIP2_318	9700
315	2101	3887	5673	784CIP2_319	9716
316	2102	3888	5674	784CIP2_320	9721
317	2103	3889	5675	784CIP2_321	9870
318	2104	3890	5676	784CIP2_322	9887
319	2105	3891	5677	784CIP2_323	9923
320	2106	3892	5678	784CIP2_324	9938
321	2107	3893	5679	784CIP2_325	9964
322	2108	3894	5680	784CIP2_326	10007
323	2109	3895	5681	784CIP2_327	10009
324	2110	3896	5682	784CIP2_328	10046
325	2111	3897	5683	784CIP2_329	10156
326	2112	3898	5684	784CIP2_330	10276
327	2113	3899	5685	784CIP2_331	10283
328	2114	3900	5686	784CIP2B_1	152
329	2115	3901	5687	784CIP2B_2	167
330	2116	3902	5688	784CIP2B_3	205
331	2117	3903	5689	784CIP2B_4	210
332	2118	3904	5690	784CIP2B_5	225
333	2119	3905	5691	784CIP2B_6	226
334	2120	3906	5692	784CIP2B_7	264
335	2121	3907	5693	784CIP2B_8	268
336	2122	3908	5694	784CIP2B_9	293
337	2123	3909	5695	784CIP2B_10	293
338	2124	3910	5696	784CIP2B_11	293
339	2125	3911	5697	784CIP2B_12	302
340	2126	3912	5698	784CIP2B_13	311
341	2127	3913	5699	784CIP2B_14	352
342	2128	3914	5700	784CIP2B_15	358
343	2129	3915	5701	784CIP2B_16	368
344	2130	3916	5702	784CIP2B_17	393
345	2131	3917	5703	784CIP2B_18	477
346	2132	3918	5704	784CIP2B_19	508
347	2133	3919	5705	784CIP2B_20	508
348	2134	3920	5706	784CIP2B_21	515
349	2135	3921	5707	784CIP2B_22	578
350	2136	3922	5708	784CIP2B_23	588
351	2137	3923	5709	784CIP2B_24	591
352	2138	3924	5710	784CIP2B_25	593
353	2139	3925	5711	784CIP2B_26	594
354	2140	3926	5712	784CIP2B_27	619
355	2141	3927	5713	784CIP2B_28	620
356	2142	3928	5714	784CIP2B_29	654
357	2143	3929	5715	784CIP2B_30	692
358	2144	3930	5716	784CIP2B_31	753
359	2145	3931	5717	784CIP2B_32	758
360	2146	3932	5718	784CIP2B_33	787
361	2147	3933	5719	784CIP2B_34	833
362	2148	3934	5720	784CIP2B_35	838
363	2149	3935	5721	784CIP2B_36	870
364	2150	3936	5722	784CIP2B_37	891
365	2151	3937	5723	784CIP2B_38	891
366	2152	3938	5724	784CIP2B_39	921
367	2153	3939	5725	784CIP2B_40	924
368	2154	3940	5726	784CIP2B_41	932
369	2155	3941	5727	784CIP2B_42	942

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
370	2156	3942	5728	784CIP2B_43	958
371	2157	3943	5729	784CIP2B_44	968
372	2158	3944	5730	784CIP2B_45	992
373	2159	3945	5731	784CIP2B_46	1025
374	2160	3946	5732	784CIP2B_47	1074
375	2161	3947	5733	784CIP2B_48	1104
376	2162	3948	5734	784CIP2B_49	1114
377	2163	3949	5735	784CIP2B_50	1144
378	2164	3950	5736	784CIP2B_51	1262
379	2165	3951	5737	784CIP2B_52	1318
380	2166	3952	5738	784CIP2B_53	1319
381	2167	3953	5739	784CIP2B_54	1328
382	2168	3954	5740	784CIP2B_55	1436
383	2169	3955	5741	784CIP2B_56	1464
384	2170	3956	5742	784CIP2B_57	1584
385	2171	3957	5743	784CIP2B_58	1617
386	2172	3958	5744	784CIP2B_59	1724
387	2173	3959	5745	784CIP2B_60	1728
388	2174	3960	5746	784CIP2B_61	1772
389	2175	3961	5747	784CIP2B_62	1809
390	2176	3962	5748	784CIP2B_63	1868
391	2177	3963	5749	784CIP2B_64	1898
392	2178	3964	5750	784CIP2B_65	1926
393	2179	3965	5751	784CIP2B_66	1965
394	2180	3966	5752	784CIP2B_67	1967
395	2181	3967	5753	784CIP2B_68	1995
396	2182	3968	5754	784CIP2B_69	2005
397	2183	3969	5755	784CIP2B_70	2027
398	2184	3970	5756	784CIP2B_71	2055
399	2185	3971	5757	784CIP2B_72	2103
400	2186	3972	5758	784CIP2B_73	2106
401	2187	3973	5759	784CIP2B_74	2166
402	2188	3974	5760	784CIP2B_75	2175
403	2189	3975	5761	784CIP2B_76	2176
404	2190	3976	5762	784CIP2B_78	2236
405	2191	3977	5763	784CIP2B_79	2250
406	2192	3978	5764	784CIP2B_80	2300
407	2193	3979	5765	784CIP2B_81	2323
408	2194	3980	5766	784CIP2B_82	2340
409	2195	3981	5767	784CIP2B_83	2371
410	2196	3982	5768	784CIP2B_84	2399
411	2197	3983	5769	784CIP2B_85	2411
412	2198	3984	5770	784CIP2B_86	2428
413	2199	3985	5771	784CIP2B_87	2430
414	2200	3986	5772	784CIP2B_88	2439
415	2201	3987	5773	784CIP2B_89	2447
416	2202	3988	5774	784CIP2B_90	2461
417	2203	3989	5775	784CIP2B_91	2487
418	2204	3990	5776	784CIP2B_92	2492
419	2205	3991	5777	784CIP2B_93	2512
420	2206	3992	5778	784CIP2B_94	2564
421	2207	3993	5779	784CIP2B_95	2678
422	2208	3994	5780	784CIP2B_96	2816
423	2209	3995	5781	784CIP2B_97	2818
424	2210	3996	5782	784CIP2B_98	2819
425	2211	3997	5783	784CIP2B_99	2943
426	2212	3998	5784	784CIP2B_100	3137
427	2213	3999	5785	784CIP2B_101	3137
428	2214	4000	5786	784CIP2B_102	3160
429	2215	4001	5787	784CIP2B_103	3323
430	2216	4002	5788	784CIP2B_104	3360
431	2217	4003	5789	784CIP2B_105	3362

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
432	2218	4004	5790	784CIP2B_106	3417
433	2219	4005	5791	784CIP2B_107	3418
434	2220	4006	5792	784CIP2B_108	3442
435	2221	4007	5793	784CIP2B_109	3442
436	2222	4008	5794	784CIP2B_110	3444
437	2223	4009	5795	784CIP2B_111	3855
438	2224	4010	5796	784CIP2B_112	3863
439	2225	4011	5797	784CIP2B_113	4090
440	2226	4012	5798	784CIP2B_114	4105
441	2227	4013	5799	784CIP2B_115	4142
442	2228	4014	5800	784CIP2B_116	4142
443	2229	4015	5801	784CIP2B_117	4149
444	2230	4016	5802	784CIP2B_118	4196
445	2231	4017	5803	784CIP2B_119	4202
446	2232	4018	5804	784CIP2B_120	4274
447	2233	4019	5805	784CIP2B_121	4304
448	2234	4020	5806	784CIP2B_122	4306
449	2235	4021	5807	784CIP2B_123	4311
450	2236	4022	5808	784CIP2B_124	4321
451	2237	4023	5809	784CIP2B_125	4323
452	2238	4024	5810	784CIP2B_126	4332
453	2239	4025	5811	784CIP2B_127	4488
454	2240	4026	5812	784CIP2B_128	4588
455	2241	4027	5813	784CIP2B_129	5569
456	2242	4028	5814	784CIP2B_130	5573
457	2243	4029	5815	784CIP2B_131	5577
458	2244	4030	5816	784CIP2B_132	5579
459	2245	4031	5817	784CIP2B_133	5582
460	2246	4032	5818	784CIP2B_134	5583
461	2247	4033	5819	784CIP2B_135	5584
462	2248	4034	5820	784CIP2B_136	5585
463	2249	4035	5821	784CIP2B_137	5591
464	2250	4036	5822	784CIP2B_138	5593
465	2251	4037	5823	784CIP2B_139	5594
466	2252	4038	5824	784CIP2B_140	5594
467	2253	4039	5825	784CIP2B_141	5598
468	2254	4040	5826	784CIP2B_142	5602
469	2255	4041	5827	784CIP2B_143	5605
470	2256	4042	5828	784CIP2B_144	5608
471	2257	4043	5829	784CIP2B_145	5617
472	2258	4044	5830	784CIP2B_146	5620
473	2259	4045	5831	784CIP2B_147	5622
474	2260	4046	5832	784CIP2B_148	5623
475	2261	4047	5833	784CIP2B_149	5624
476	2262	4048	5834	784CIP2B_150	5625
477	2263	4049	5835	784CIP2B_151	5627
478	2264	4050	5836	784CIP2B_152	5628
479	2265	4051	5837	784CIP2B_153	5630
480	2266	4052	5838	784CIP2B_154	5632
481	2267	4053	5839	784CIP2B_155	5640
482	2268	4054	5840	784CIP2B_156	5641
483	2269	4055	5841	784CIP2B_157	5643
484	2270	4056	5842	784CIP2B_158	5647
485	2271	4057	5843	784CIP2B_159	5649
486	2272	4058	5844	784CIP2B_160	5658
487	2273	4059	5845	784CIP2B_161	5659
488	2274	4060	5846	784CIP2B_162	5667
489	2275	4061	5847	784CIP2B_163	5672
490	2276	4062	5848	784CIP2B_164	5674
491	2277	4063	5849	784CIP2B_165	5678
492	2278	4064	5850	784CIP2B_166	5680
493	2279	4065	5851	784CIP2B_167	5684

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
494	2280	4066	5852	784CIP2B_168	5686
495	2281	4067	5853	784CIP2B_169	5694
496	2282	4068	5854	784CIP2B_170	5698
497	2283	4069	5855	784CIP2B_171	5699
498	2284	4070	5856	784CIP2B_172	5712
499	2285	4071	5857	784CIP2B_173	5719
500	2286	4072	5858	784CIP2B_174	5720
501	2287	4073	5859	784CIP2B_175	5727
502	2288	4074	5860	784CIP2B_176	5730
503	2289	4075	5861	784CIP2B_177	5734
504	2290	4076	5862	784CIP2B_178	5738
505	2291	4077	5863	784CIP2B_179	5739
506	2292	4078	5864	784CIP2B_180	5740
507	2293	4079	5865	784CIP2B_181	5744
508	2294	4080	5866	784CIP2B_182	5748
509	2295	4081	5867	784CIP2B_183	5749
510	2296	4082	5868	784CIP2B_184	5750
511	2297	4083	5869	784CIP2B_185	5750
512	2298	4084	5870	784CIP2B_186	5750
513	2299	4085	5871	784CIP2B_187	5761
514	2300	4086	5872	784CIP2B_188	5762
515	2301	4087	5873	784CIP2B_189	5767
516	2302	4088	5874	784CIP2B_190	5773
517	2303	4089	5875	784CIP2B_191	5783
518	2304	4090	5876	784CIP2B_192	5784
519	2305	4091	5877	784CIP2B_193	5788
520	2306	4092	5878	784CIP2B_194	5798
521	2307	4093	5879	784CIP2B_196	5807
522	2308	4094	5880	784CIP2B_197	5818
523	2309	4095	5881	784CIP2B_198	5819
524	2310	4096	5882	784CIP2B_199	5827
525	2311	4097	5883	784CIP2B_200	5828
526	2312	4098	5884	784CIP2B_201	5842
527	2313	4099	5885	784CIP2B_202	5853
528	2314	4100	5886	784CIP2B_203	5861
529	2315	4101	5887	784CIP2B_204	5864
530	2316	4102	5888	784CIP2B_205	5865
531	2317	4103	5889	784CIP2B_206	5871
532	2318	4104	5890	784CIP2B_207	5873
533	2319	4105	5891	784CIP2B_208	5873
534	2320	4106	5892	784CIP2B_209	5875
535	2321	4107	5893	784CIP2B_210	5878
536	2322	4108	5894	784CIP2B_211	5879
537	2323	4109	5895	784CIP2B_212	5880
538	2324	4110	5896	784CIP2B_213	5880
539	2325	4111	5897	784CIP2B_214	5880
540	2326	4112	5898	784CIP2B_215	5880
541	2327	4113	5899	784CIP2B_216	5885
542	2328	4114	5900	784CIP2B_217	5895
543	2329	4115	5901	784CIP2B_218	5898
544	2330	4116	5902	784CIP2B_219	5902
545	2331	4117	5903	784CIP2B_220	5904
546	2332	4118	5904	784CIP2B_221	5918
547	2333	4119	5905	784CIP2B_222	5921
548	2334	4120	5906	784CIP2B_223	5927
549	2335	4121	5907	784CIP2B_224	5932
550	2336	4122	5908	784CIP2B_225	5939
551	2337	4123	5909	784CIP2B_226	5945
552	2338	4124	5910	784CIP2B_227	5946
553	2339	4125	5911	784CIP2B_228	5947
554	2340	4126	5912	784CIP2B_229	5956
555	2341	4127	5913	784CIP2B_230	5967

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
556	2342	4128	5914	784CIP2B_232	5975
557	2343	4129	5915	784CIP2B_233	5977
558	2344	4130	5916	784CIP2B_234	5978
559	2345	4131	5917	784CIP2B_235	5979
560	2346	4132	5918	784CIP2B_236	5980
561	2347	4133	5919	784CIP2B_237	5988
562	2348	4134	5920	784CIP2B_238	5989
563	2349	4135	5921	784CIP2B_239	5991
564	2350	4136	5922	784CIP2B_240	5997
565	2351	4137	5923	784CIP2B_241	5998
566	2352	4138	5924	784CIP2B_242	6003
567	2353	4139	5925	784CIP2B_243	6004
568	2354	4140	5926	784CIP2B_244	6013
569	2355	4141	5927	784CIP2B_245	6028
570	2356	4142	5928	784CIP2B_246	6028
571	2357	4143	5929	784CIP2B_247	6029
572	2358	4144	5930	784CIP2B_248	6031
573	2359	4145	5931	784CIP2B_249	6031
574	2360	4146	5932	784CIP2B_250	6032
575	2361	4147	5933	784CIP2B_251	6037
576	2362	4148	5934	784CIP2B_252	6037
577	2363	4149	5935	784CIP2B_253	6043
578	2364	4150	5936	784CIP2B_254	6044
579	2365	4151	5937	784CIP2B_255	6046
580	2366	4152	5938	784CIP2B_256	6048
581	2367	4153	5939	784CIP2B_257	6049
582	2368	4154	5940	784CIP2B_258	6051
583	2369	4155	5941	784CIP2B_259	6053
584	2370	4156	5942	784CIP2B_260	6060
585	2371	4157	5943	784CIP2B_261	6063
586	2372	4158	5944	784CIP2B_262	6066
587	2373	4159	5945	784CIP2B_263	6067
588	2374	4160	5946	784CIP2B_264	6068
589	2375	4161	5947	784CIP2B_265	6073
590	2376	4162	5948	784CIP2B_266	6076
591	2377	4163	5949	784CIP2B_267	6076
592	2378	4164	5950	784CIP2B_268	6077
593	2379	4165	5951	784CIP2B_269	6079
594	2380	4166	5952	784CIP2B_270	6082
595	2381	4167	5953	784CIP2B_272	6088
596	2382	4168	5954	784CIP2B_273	6091
597	2383	4169	5955	784CIP2B_274	6094
598	2384	4170	5956	784CIP2B_275	6101
599	2385	4171	5957	784CIP2B_276	6103
600	2386	4172	5958	784CIP2B_277	6104
601	2387	4173	5959	784CIP2B_278	6108
602	2388	4174	5960	784CIP2B_279	6112
603	2389	4175	5961	784CIP2B_280	6121
604	2390	4176	5962	784CIP2B_281	6125
605	2391	4177	5963	784CIP2B_282	6126
606	2392	4178	5964	784CIP2B_283	6128
607	2393	4179	5965	784CIP2B_284	6129
608	2394	4180	5966	784CIP2B_285	6133
609	2395	4181	5967	784CIP2B_286	6133
610	2396	4182	5968	784CIP2B_287	6135
611	2397	4183	5969	784CIP2B_288	6139
612	2398	4184	5970	784CIP2B_289	6141
613	2399	4185	5971	784CIP2B_290	6145
614	2400	4186	5972	784CIP2B_291	6146
615	2401	4187	5973	784CIP2B_292	6148
616	2402	4188	5974	784CIP2B_293	6149
617	2403	4189	5975	784CIP2B_294	6149

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
618	2404	4190	5976	784CIP2B_295	6153
619	2405	4191	5977	784CIP2B_296	6159
620	2406	4192	5978	784CIP2B_297	6164
621	2407	4193	5979	784CIP2B_298	6167
622	2408	4194	5980	784CIP2B_299	6172
623	2409	4195	5981	784CIP2B_300	6173
624	2410	4196	5982	784CIP2B_301	6190
625	2411	4197	5983	784CIP2B_302	6194
626	2412	4198	5984	784CIP2B_303	6196
627	2413	4199	5985	784CIP2B_304	6197
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629	2415	4201	5987	784CIP2B_306	6198
630	2416	4202	5988	784CIP2B_308	6214
631	2417	4203	5989	784CIP2B_309	6215
632	2418	4204	5990	784CIP2B_310	6219
633	2419	4205	5991	784CIP2B_311	6226
634	2420	4206	5992	784CIP2B_312	6229
635	2421	4207	5993	784CIP2B_313	6234
636	2422	4208	5994	784CIP2B_314	6237
637	2423	4209	5995	784CIP2B_315	6238
638	2424	4210	5996	784CIP2B_316	6239
639	2425	4211	5997	784CIP2B_317	6239
640	2426	4212	5998	784CIP2B_318	6239
641	2427	4213	5999	784CIP2B_319	6240
642	2428	4214	6000	784CIP2B_320	6244
643	2429	4215	6001	784CIP2B_321	6245
644	2430	4216	6002	784CIP2B_322	6250
645	2431	4217	6003	784CIP2B_323	6252
646	2432	4218	6004	784CIP2B_324	6252
647	2433	4219	6005	784CIP2B_325	6256
648	2434	4220	6006	784CIP2B_326	6260
649	2435	4221	6007	784CIP2B_327	6261
650	2436	4222	6008	784CIP2B_328	6264
651	2437	4223	6009	784CIP2B_329	6265
652	2438	4224	6010	784CIP2B_330	6266
653	2439	4225	6011	784CIP2B_331	6270
654	2440	4226	6012	784CIP2B_332	6271
655	2441	4227	6013	784CIP2B_334	6274
656	2442	4228	6014	784CIP2B_335	6276
657	2443	4229	6015	784CIP2B_336	6281
658	2444	4230	6016	784CIP2B_337	6281
659	2445	4231	6017	784CIP2B_338	6288
660	2446	4232	6018	784CIP2B_339	6292
661	2447	4233	6019	784CIP2B_340	6294
662	2448	4234	6020	784CIP2B_343	6312
663	2449	4235	6021	784CIP2B_344	6312
664	2450	4236	6022	784CIP2B_345	6312
665	2451	4237	6023	784CIP2B_346	6322
666	2452	4238	6024	784CIP2B_347	6324
667	2453	4239	6025	784CIP2B_349	6329
668	2454	4240	6026	784CIP2B_350	6331
669	2455	4241	6027	784CIP2B_351	6333
670	2456	4242	6028	784CIP2B_352	6334
671	2457	4243	6029	784CIP2B_353	6337
672	2458	4244	6030	784CIP2B_354	6339
673	2459	4245	6031	784CIP2B_355	6346
674	2460	4246	6032	784CIP2B_356	6348
675	2461	4247	6033	784CIP2B_357	6348
676	2462	4248	6034	784CIP2B_358	6350
677	2463	4249	6035	784CIP2B_359	6351
678	2464	4250	6036	784CIP2B_360	6355
679	2465	4251	6037	784CIP2B_361	6362

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
680	2466	4252	6038	784CIP2B_362	6368
681	2467	4253	6039	784CIP2B_363	6369
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683	2469	4255	6041	784CIP2B_365	6376
684	2470	4256	6042	784CIP2B_366	6379
685	2471	4257	6043	784CIP2B_367	6380
686	2472	4258	6044	784CIP2B_368	6381
687	2473	4259	6045	784CIP2B_369	6392
688	2474	4260	6046	784CIP2B_370	6395
689	2475	4261	6047	784CIP2B_371	6397
690	2476	4262	6048	784CIP2B_372	6400
691	2477	4263	6049	784CIP2B_373	6401
692	2478	4264	6050	784CIP2B_374	6411
693	2479	4265	6051	784CIP2B_375	6411
694	2480	4266	6052	784CIP2B_376	6411
695	2481	4267	6053	784CIP2B_377	6416
696	2482	4268	6054	784CIP2B_378	6418
697	2483	4269	6055	784CIP2B_379	6422
698	2484	4270	6056	784CIP2B_380	6423
699	2485	4271	6057	784CIP2B_381	6426
700	2486	4272	6058	784CIP2B_382	6427
701	2487	4273	6059	784CIP2B_383	6428
702	2488	4274	6060	784CIP2B_384	6429
703	2489	4275	6061	784CIP2B_385	6430
704	2490	4276	6062	784CIP2B_386	6432
705	2491	4277	6063	784CIP2B_387	6432
706	2492	4278	6064	784CIP2B_388	6438
707	2493	4279	6065	784CIP2B_389	6441
708	2494	4280	6066	784CIP2B_390	6446
709	2495	4281	6067	784CIP2B_391	6454
710	2496	4282	6068	784CIP2B_392	6459
711	2497	4283	6069	784CIP2B_394	6461
712	2498	4284	6070	784CIP2B_395	6467
713	2499	4285	6071	784CIP2B_396	6468
714	2500	4286	6072	784CIP2B_397	6487
715	2501	4287	6073	784CIP2B_398	6491
716	2502	4288	6074	784CIP2B_399	6506
717	2503	4289	6075	784CIP2B_401	6514
718	2504	4290	6076	784CIP2B_402	6519
719	2505	4291	6077	784CIP2B_403	6521
720	2506	4292	6078	784CIP2B_404	6532
721	2507	4293	6079	784CIP2B_405	6536
722	2508	4294	6080	784CIP2B_406	6543
723	2509	4295	6081	784CIP2B_407	6544
724	2510	4296	6082	784CIP2B_408	6548
725	2511	4297	6083	784CIP2B_409	6551
726	2512	4298	6084	784CIP2B_410	6551
727	2513	4299	6085	784CIP2B_411	6552
728	2514	4300	6086	784CIP2B_412	6554
729	2515	4301	6087	784CIP2B_413	6556
730	2516	4302	6088	784CIP2B_414	6560
731	2517	4303	6089	784CIP2B_415	6563
732	2518	4304	6090	784CIP2B_416	6564
733	2519	4305	6091	784CIP2B_417	6567
734	2520	4306	6092	784CIP2B_418	6573
735	2521	4307	6093	784CIP2B_419	6575
736	2522	4308	6094	784CIP2B_420	6577
737	2523	4309	6095	784CIP2B_421	6593
738	2524	4310	6096	784CIP2B_422	6595
739	2525	4311	6097	784CIP2B_423	6599
740	2526	4312	6098	784CIP2B_424	6625
741	2527	4313	6099	784CIP2B_425	6625

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
742	2528	4314	6100	784CIP2B_426	6626
743	2529	4315	6101	784CIP2B_427	6630
744	2530	4316	6102	784CIP2B_428	6631
745	2531	4317	6103	784CIP2B_429	6632
746	2532	4318	6104	784CIP2B_430	6633
747	2533	4319	6105	784CIP2B_431	6634
748	2534	4320	6106	784CIP2B_432	6638
749	2535	4321	6107	784CIP2B_433	6641
750	2536	4322	6108	784CIP2B_434	6644
751	2537	4323	6109	784CIP2B_435	6646
752	2538	4324	6110	784CIP2B_436	6648
753	2539	4325	6111	784CIP2B_437	6652
754	2540	4326	6112	784CIP2B_438	6654
755	2541	4327	6113	784CIP2B_439	6657
756	2542	4328	6114	784CIP2B_440	6658
757	2543	4329	6115	784CIP2B_441	6663
758	2544	4330	6116	784CIP2B_442	6664
759	2545	4331	6117	784CIP2B_443	6668
760	2546	4332	6118	784CIP2B_444	6669
761	2547	4333	6119	784CIP2B_445	6673
762	2548	4334	6120	784CIP2B_446	6685
763	2549	4335	6121	784CIP2B_447	6687
764	2550	4336	6122	784CIP2B_448	6689
765	2551	4337	6123	784CIP2B_449	6693
766	2552	4338	6124	784CIP2B_450	6698
767	2553	4339	6125	784CIP2B_451	6699
768	2554	4340	6126	784CIP2B_452	6705
769	2555	4341	6127	784CIP2B_453	6711
770	2556	4342	6128	784CIP2B_454	6713
771	2557	4343	6129	784CIP2B_455	6716
772	2558	4344	6130	784CIP2B_456	6725
773	2559	4345	6131	784CIP2B_457	6726
774	2560	4346	6132	784CIP2B_458	6727
775	2561	4347	6133	784CIP2B_459	6730
776	2562	4348	6134	784CIP2B_460	6730
777	2563	4349	6135	784CIP2B_461	6730
778	2564	4350	6136	784CIP2B_462	6732
779	2565	4351	6137	784CIP2B_463	6733
780	2566	4352	6138	784CIP2B_464	6737
781	2567	4353	6139	784CIP2B_465	6745
782	2568	4354	6140	784CIP2B_466	6751
783	2569	4355	6141	784CIP2B_467	6754
784	2570	4356	6142	784CIP2B_468	6758
785	2571	4357	6143	784CIP2B_469	6761
786	2572	4358	6144	784CIP2B_470	6765
787	2573	4359	6145	784CIP2B_471	6768
788	2574	4360	6146	784CIP2B_472	6773
789	2575	4361	6147	784CIP2B_473	6776
790	2576	4362	6148	784CIP2B_474	6796
791	2577	4363	6149	784CIP2B_475	6798
792	2578	4364	6150	784CIP2B_476	6823
793	2579	4365	6151	784CIP2B_477	6825
794	2580	4366	6152	784CIP2B_478	6826
795	2581	4367	6153	784CIP2B_479	6839
796	2582	4368	6154	784CIP2B_480	6844
797	2583	4369	6155	784CIP2B_482	6849
798	2584	4370	6156	784CIP2B_483	6854
799	2585	4371	6157	784CIP2B_484	6857
800	2586	4372	6158	784CIP2B_485	6861
801	2587	4373	6159	784CIP2B_486	6873
802	2588	4374	6160	784CIP2B_487	6875
803	2589	4375	6161	784CIP2B_488	6877

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
804	2590	4376	6162	784CIP2B_489	6880
805	2591	4377	6163	784CIP2B_490	6885
806	2592	4378	6164	784CIP2B_491	6890
807	2593	4379	6165	784CIP2B_492	6890
808	2594	4380	6166	784CIP2B_493	6894
809	2595	4381	6167	784CIP2B_494	6901
810	2596	4382	6168	784CIP2B_495	6904
811	2597	4383	6169	784CIP2B_496	6907
812	2598	4384	6170	784CIP2B_497	6914
813	2599	4385	6171	784CIP2B_498	6917
814	2600	4386	6172	784CIP2B_499	6923
815	2601	4387	6173	784CIP2B_500	6929
816	2602	4388	6174	784CIP2B_501	6931
817	2603	4389	6175	784CIP2B_502	6935
818	2604	4390	6176	784CIP2B_503	6940
819	2605	4391	6177	784CIP2B_504	6945
820	2606	4392	6178	784CIP2B_505	6946
821	2607	4393	6179	784CIP2B_506	6947
822	2608	4394	6180	784CIP2B_507	6949
823	2609	4395	6181	784CIP2B_508	6959
824	2610	4396	6182	784CIP2B_509	6960
825	2611	4397	6183	784CIP2B_510	6962
826	2612	4398	6184	784CIP2B_511	6963
827	2613	4399	6185	784CIP2B_512	6967
828	2614	4400	6186	784CIP2B_513	6983
829	2615	4401	6187	784CIP2B_514	6988
830	2616	4402	6188	784CIP2B_515	6996
831	2617	4403	6189	784CIP2B_516	7003
832	2618	4404	6190	784CIP2B_517	7016
833	2619	4405	6191	784CIP2B_518	7017
834	2620	4406	6192	784CIP2B_519	7025
835	2621	4407	6193	784CIP2B_520	7025
836	2622	4408	6194	784CIP2B_521	7025
837	2623	4409	6195	784CIP2B_522	7050
838	2624	4410	6196	784CIP2B_523	7051
839	2625	4411	6197	784CIP2B_524	7055
840	2626	4412	6198	784CIP2B_525	7060
841	2627	4413	6199	784CIP2B_526	7064
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843	2629	4415	6201	784CIP2B_528	7071
844	2630	4416	6202	784CIP2B_529	7072
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846	2632	4418	6204	784CIP2B_531	7076
847	2633	4419	6205	784CIP2B_532	7088
848	2634	4420	6206	784CIP2B_533	7089
849	2635	4421	6207	784CIP2B_534	7091
850	2636	4422	6208	784CIP2B_535	7091
851	2637	4423	6209	784CIP2B_536	7104
852	2638	4424	6210	784CIP2B_537	7105
853	2639	4425	6211	784CIP2B_538	7105
854	2640	4426	6212	784CIP2B_539	7109
855	2641	4427	6213	784CIP2B_540	7109
856	2642	4428	6214	784CIP2B_541	7119
857	2643	4429	6215	784CIP2B_542	7120
858	2644	4430	6216	784CIP2B_543	7121
859	2645	4431	6217	784CIP2B_544	7126
860	2646	4432	6218	784CIP2B_545	7127
861	2647	4433	6219	784CIP2B_546	7130
862	2648	4434	6220	784CIP2B_547	7131
863	2649	4435	6221	784CIP2B_548	7144
864	2650	4436	6222	784CIP2B_549	7159
865	2651	4437	6223	784CIP2B_550	7163

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
866	2652	4438	6224	784CIP2B_551	7175
867	2653	4439	6225	784CIP2B_552	7188
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869	2655	4441	6227	784CIP2B_554	7190
870	2656	4442	6228	784CIP2B_555	7191
871	2657	4443	6229	784CIP2B_556	7203
872	2658	4444	6230	784CIP2B_557	7204
873	2659	4445	6231	784CIP2B_558	7208
874	2660	4446	6232	784CIP2B_559	7209
875	2661	4447	6233	784CIP2B_560	7210
876	2662	4448	6234	784CIP2B_561	7216
877	2663	4449	6235	784CIP2B_562	7221
878	2664	4450	6236	784CIP2B_563	7230
879	2665	4451	6237	784CIP2B_564	7237
880	2666	4452	6238	784CIP2B_565	7240
881	2667	4453	6239	784CIP2B_566	7245
882	2668	4454	6240	784CIP2B_567	7250
883	2669	4455	6241	784CIP2B_568	7251
884	2670	4456	6242	784CIP2B_569	7255
885	2671	4457	6243	784CIP2B_570	7260
886	2672	4458	6244	784CIP2B_571	7265
887	2673	4459	6245	784CIP2B_572	7268
888	2674	4460	6246	784CIP2B_573	7275
889	2675	4461	6247	784CIP2B_574	7279
890	2676	4462	6248	784CIP2B_575	7283
891	2677	4463	6249	784CIP2B_576	7283
892	2678	4464	6250	784CIP2B_577	7287
893	2679	4465	6251	784CIP2B_578	7301
894	2680	4466	6252	784CIP2B_579	7308
895	2681	4467	6253	784CIP2B_580	7308
896	2682	4468	6254	784CIP2B_581	7309
897	2683	4469	6255	784CIP2B_582	7319
898	2684	4470	6256	784CIP2B_583	7320
899	2685	4471	6257	784CIP2B_584	7326
900	2686	4472	6258	784CIP2B_585	7326
901	2687	4473	6259	784CIP2B_586	7334
902	2688	4474	6260	784CIP2B_587	7337
903	2689	4475	6261	784CIP2B_588	7339
904	2690	4476	6262	784CIP2B_589	7344
905	2691	4477	6263	784CIP2B_590	7355
906	2692	4478	6264	784CIP2B_591	7363
907	2693	4479	6265	784CIP2B_592	7363
908	2694	4480	6266	784CIP2B_593	7365
909	2695	4481	6267	784CIP2B_594	7368
910	2696	4482	6268	784CIP2B_595	7369
911	2697	4483	6269	784CIP2B_596	7372
912	2698	4484	6270	784CIP2B_599	7375
913	2699	4485	6271	784CIP2B_600	7381
914	2700	4486	6272	784CIP2B_601	7383
915	2701	4487	6273	784CIP2B_602	7387
916	2702	4488	6274	784CIP2B_603	7391
917	2703	4489	6275	784CIP2B_604	7393
918	2704	4490	6276	784CIP2B_605	7395
919	2705	4491	6277	784CIP2B_606	7397
920	2706	4492	6278	784CIP2B_607	7399
921	2707	4493	6279	784CIP2B_608	7405
922	2708	4494	6280	784CIP2B_609	7406
923	2709	4495	6281	784CIP2B_610	7406
924	2710	4496	6282	784CIP2B_611	7409
925	2711	4497	6283	784CIP2B_612	7410
926	2712	4498	6284	784CIP2B_613	7411
927	2713	4499	6285	784CIP2B_614	7417

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
928	2714	4500	6286	784CIP2B_615	7418
929	2715	4501	6287	784CIP2B_616	7421
930	2716	4502	6288	784CIP2B_617	7422
931	2717	4503	6289	784CIP2B_618	7422
932	2718	4504	6290	784CIP2B_619	7423
933	2719	4505	6291	784CIP2B_620	7424
934	2720	4506	6292	784CIP2B_621	7426
935	2721	4507	6293	784CIP2B_622	7427
936	2722	4508	6294	784CIP2B_623	7428
937	2723	4509	6295	784CIP2B_624	7430
938	2724	4510	6296	784CIP2B_625	7435
939	2725	4511	6297	784CIP2B_626	7437
940	2726	4512	6298	784CIP2B_627	7439
941	2727	4513	6299	784CIP2B_628	7440
942	2728	4514	6300	784CIP2B_629	7442
943	2729	4515	6301	784CIP2B_630	7450
944	2730	4516	6302	784CIP2B_631	7451
945	2731	4517	6303	784CIP2B_632	7452
946	2732	4518	6304	784CIP2B_633	7454
947	2733	4519	6305	784CIP2B_634	7457
948	2734	4520	6306	784CIP2B_635	7459
949	2735	4521	6307	784CIP2B_636	7461
950	2736	4522	6308	784CIP2B_637	7463
951	2737	4523	6309	784CIP2B_638	7466
952	2738	4524	6310	784CIP2B_639	7469
953	2739	4525	6311	784CIP2B_640	7473
954	2740	4526	6312	784CIP2B_641	7481
955	2741	4527	6313	784CIP2B_642	7482
956	2742	4528	6314	784CIP2B_643	7482
957	2743	4529	6315	784CIP2B_644	7483
958	2744	4530	6316	784CIP2B_645	7485
959	2745	4531	6317	784CIP2B_646	7486
960	2746	4532	6318	784CIP2B_647	7487
961	2747	4533	6319	784CIP2B_648	7491
962	2748	4534	6320	784CIP2B_649	7492
963	2749	4535	6321	784CIP2B_650	7494
964	2750	4536	6322	784CIP2B_651	7498
965	2751	4537	6323	784CIP2B_652	7504
966	2752	4538	6324	784CIP2B_653	7508
967	2753	4539	6325	784CIP2B_654	7516
968	2754	4540	6326	784CIP2B_655	7518
969	2755	4541	6327	784CIP2B_656	7519
970	2756	4542	6328	784CIP2B_657	7521
971	2757	4543	6329	784CIP2B_658	7529
972	2758	4544	6330	784CIP2B_659	7532
973	2759	4545	6331	784CIP2B_660	7533
974	2760	4546	6332	784CIP2B_661	7535
975	2761	4547	6333	784CIP2B_662	7545
976	2762	4548	6334	784CIP2B_663	7546
977	2763	4549	6335	784CIP2B_664	7552
978	2764	4550	6336	784CIP2B_665	7554
979	2765	4551	6337	784CIP2B_666	7567
980	2766	4552	6338	784CIP2B_667	7569
981	2767	4553	6339	784CIP2B_668	7575
982	2768	4554	6340	784CIP2B_669	7576
983	2769	4555	6341	784CIP2B_670	7577
984	2770	4556	6342	784CIP2B_671	7579
985	2771	4557	6343	784CIP2B_672	7582
986	2772	4558	6344	784CIP2B_673	7587
987	2773	4559	6345	784CIP2B_674	7589
988	2774	4560	6346	784CIP2B_675	7597
989	2775	4561	6347	784CIP2B_676	7597

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
990	2776	4562	6348	784CIP2B_677	7609
991	2777	4563	6349	784CIP2B_678	7609
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993	2779	4565	6351	784CIP2B_680	7613
994	2780	4566	6352	784CIP2B_681	7623
995	2781	4567	6353	784CIP2B_682	7629
996	2782	4568	6354	784CIP2B_683	7630
997	2783	4569	6355	784CIP2B_684	7633
998	2784	4570	6356	784CIP2B_685	7635
999	2785	4571	6357	784CIP2B_686	7638
1000	2786	4572	6358	784CIP2B_687	7639
1001	2787	4573	6359	784CIP2B_688	7646
1002	2788	4574	6360	784CIP2B_689	7647
1003	2789	4575	6361	784CIP2B_690	7648
1004	2790	4576	6362	784CIP2B_691	7658
1005	2791	4577	6363	784CIP2B_692	7664
1006	2792	4578	6364	784CIP2B_693	7664
1007	2793	4579	6365	784CIP2B_695	7674
1008	2794	4580	6366	784CIP2B_696	7675
1009	2795	4581	6367	784CIP2B_697	7676
1010	2796	4582	6368	784CIP2B_698	7681
1011	2797	4583	6369	784CIP2B_699	7688
1012	2798	4584	6370	784CIP2B_700	7693
1013	2799	4585	6371	784CIP2B_701	7694
1014	2800	4586	6372	784CIP2B_702	7715
1015	2801	4587	6373	784CIP2B_703	7716
1016	2802	4588	6374	784CIP2B_704	7718
1017	2803	4589	6375	784CIP2B_705	7721
1018	2804	4590	6376	784CIP2B_706	7723
1019	2805	4591	6377	784CIP2B_707	7729
1020	2806	4592	6378	784CIP2B_708	7733
1021	2807	4593	6379	784CIP2B_709	7735
1022	2808	4594	6380	784CIP2B_710	7741
1023	2809	4595	6381	784CIP2B_711	7743
1024	2810	4596	6382	784CIP2B_712	7748
1025	2811	4597	6383	784CIP2B_713	7749
1026	2812	4598	6384	784CIP2B_714	7750
1027	2813	4599	6385	784CIP2B_715	7757
1028	2814	4600	6386	784CIP2B_716	7759
1029	2815	4601	6387	784CIP2B_717	7760
1030	2816	4602	6388	784CIP2B_718	7760
1031	2817	4603	6389	784CIP2B_719	7764
1032	2818	4604	6390	784CIP2B_720	7765
1033	2819	4605	6391	784CIP2B_721	7766
1034	2820	4606	6392	784CIP2B_722	7767
1035	2821	4607	6393	784CIP2B_723	7769
1036	2822	4608	6394	784CIP2B_724	7770
1037	2823	4609	6395	784CIP2B_725	7774
1038	2824	4610	6396	784CIP2B_726	7779
1039	2825	4611	6397	784CIP2B_727	7781
1040	2826	4612	6398	784CIP2B_728	7782
1041	2827	4613	6399	784CIP2B_729	7783
1042	2828	4614	6400	784CIP2B_730	7787
1043	2829	4615	6401	784CIP2B_731	7792
1044	2830	4616	6402	784CIP2B_732	7795
1045	2831	4617	6403	784CIP2B_733	7801
1046	2832	4618	6404	784CIP2B_734	7807
1047	2833	4619	6405	784CIP2B_735	7808
1048	2834	4620	6406	784CIP2B_736	7819
1049	2835	4621	6407	784CIP2B_737	7824
1050	2836	4622	6408	784CIP2B_738	7826
1051	2837	4623	6409	784CIP2B_739	7829

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide. sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1052	2838	4624	6410	784CIP2B_740	7832
1053	2839	4625	6411	784CIP2B_741	7839
1054	2840	4626	6412	784CIP2B_743	7847
1055	2841	4627	6413	784CIP2B_744	7848
1056	2842	4628	6414	784CIP2B_745	7853
1057	2843	4629	6415	784CIP2B_746	7854
1058	2844	4630	6416	784CIP2B_747	7856
1059	2845	4631	6417	784CIP2B_748	7862
1060	2846	4632	6418	784CIP2B_749	7865
1061	2847	4633	6419	784CIP2B_750	7874
1062	2848	4634	6420	784CIP2B_751	7877
1063	2849	4635	6421	784CIP2B_752	7880
1064	2850	4636	6422	784CIP2B_753	7882
1065	2851	4637	6423	784CIP2B_754	7884
1066	2852	4638	6424	784CIP2B_755	7886
1067	2853	4639	6425	784CIP2B_756	7888
1068	2854	4640	6426	784CIP2B_757	7889
1069	2855	4641	6427	784CIP2B_758	7901
1070	2856	4642	6428	784CIP2B_759	7910
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1072	2858	4644	6430	784CIP2B_761	7921
1073	2859	4645	6431	784CIP2B_762	7923
1074	2860	4646	6432	784CIP2B_763	7924
1075	2861	4647	6433	784CIP2B_764	7925
1076	2862	4648	6434	784CIP2B_765	7928
1077	2863	4649	6435	784CIP2B_766	7929
1078	2864	4650	6436	784CIP2B_767	7930
1079	2865	4651	6437	784CIP2B_768	7934
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1081	2867	4653	6439	784CIP2B_770	7942
1082	2868	4654	6440	784CIP2B_771	7945
1083	2869	4655	6441	784CIP2B_772	7946
1084	2870	4656	6442	784CIP2B_773	7948
1085	2871	4657	6443	784CIP2B_774	7951
1086	2872	4658	6444	784CIP2B_775	7952
1087	2873	4659	6445	784CIP2B_776	7953
1088	2874	4660	6446	784CIP2B_777	7954
1089	2875	4661	6447	784CIP2B_778	7957
1090	2876	4662	6448	784CIP2B_779	7958
1091	2877	4663	6449	784CIP2B_780	7961
1092	2878	4664	6450	784CIP2B_781	7965
1093	2879	4665	6451	784CIP2B_782	7966
1094	2880	4666	6452	784CIP2B_783	7979
1095	2881	4667	6453	784CIP2B_784	7986
1096	2882	4668	6454	784CIP2B_785	7986
1097	2883	4669	6455	784CIP2B_786	7988
1098	2884	4670	6456	784CIP2B_787	7991
1099	2885	4671	6457	784CIP2B_788	7992
1100	2886	4672	6458	784CIP2B_789	7992
1101	2887	4673	6459	784CIP2B_790	7992
1102	2888	4674	6460	784CIP2B_791	7992
1103	2889	4675	6461	784CIP2B_792	8003
1104	2890	4676	6462	784CIP2B_793	8014
1105	2891	4677	6463	784CIP2B_794	8015
1106	2892	4678	6464	784CIP2B_795	8016
1107	2893	4679	6465	784CIP2B_796	8017
1108	2894	4680	6466	784CIP2B_797	8019
1109	2895	4681	6467	784CIP2B_798	8020
1110	2896	4682	6468	784CIP2B_799	8022
1111	2897	4683	6469	784CIP2B_800	8022
1112	2898	4684	6470	784CIP2B_801	8028
1113	2899	4685	6471	784CIP2B_802	8030

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1114	2900	4686	6472	784CIP2B_803	8038
1115	2901	4687	6473	784CIP2B_804	8042
1116	2902	4688	6474	784CIP2B_805	8045
1117	2903	4689	6475	784CIP2B_806	8045
1118	2904	4690	6476	784CIP2B_807	8046
1119	2905	4691	6477	784CIP2B_808	8047
1120	2906	4692	6478	784CIP2B_809	8051
1121	2907	4693	6479	784CIP2B_810	8059
1122	2908	4694	6480	784CIP2B_811	8064
1123	2909	4695	6481	784CIP2B_812	8069
1124	2910	4696	6482	784CIP2B_813	8074
1125	2911	4697	6483	784CIP2B_814	8077
1126	2912	4698	6484	784CIP2B_815	8078
1127	2913	4699	6485	784CIP2B_816	8079
1128	2914	4700	6486	784CIP2B_817	8084
1129	2915	4701	6487	784CIP2B_818	8088
1130	2916	4702	6488	784CIP2B_819	8090
1131	2917	4703	6489	784CIP2B_820	8091
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1134	2920	4706	6492	784CIP2B_823	8100
1135	2921	4707	6493	784CIP2B_824	8102
1136	2922	4708	6494	784CIP2B_825	8103
1137	2923	4709	6495	784CIP2B_826	8103
1138	2924	4710	6496	784CIP2B_827	8104
1139	2925	4711	6497	784CIP2B_828	8108
1140	2926	4712	6498	784CIP2B_829	8110
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1144	2930	4716	6502	784CIP2B_833	8130
1145	2931	4717	6503	784CIP2B_834	8130
1146	2932	4718	6504	784CIP2B_835	8143
1147	2933	4719	6505	784CIP2B_836	8143
1148	2934	4720	6506	784CIP2B_837	8154
1149	2935	4721	6507	784CIP2B_838	8155
1150	2936	4722	6508	784CIP2B_839	8162
1151	2937	4723	6509	784CIP2B_840	8163
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1153	2939	4725	6511	784CIP2B_842	8173
1154	2940	4726	6512	784CIP2B_843	8179
1155	2941	4727	6513	784CIP2B_844	8182
1156	2942	4728	6514	784CIP2B_845	8183
1157	2943	4729	6515	784CIP2B_846	8184
1158	2944	4730	6516	784CIP2B_847	8185
1159	2945	4731	6517	784CIP2B_848	8187
1160	2946	4732	6518	784CIP2B_849	8188
1161	2947	4733	6519	784CIP2B_850	8190
1162	2948	4734	6520	784CIP2B_851	8190
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1164	2950	4736	6522	784CIP2B_853	8193
1165	2951	4737	6523	784CIP2B_854	8197
1166	2952	4738	6524	784CIP2B_855	8197
1167	2953	4739	6525	784CIP2B_856	8199
1168	2954	4740	6526	784CIP2B_857	8202
1169	2955	4741	6527	784CIP2B_858	8203
1170	2956	4742	6528	784CIP2B_859	8208
1171	2957	4743	6529	784CIP2B_860	8209
1172	2958	4744	6530	784CIP2B_861	8211
1173	2959	4745	6531	784CIP2B_862	8214
1174	2960	4746	6532	784CIP2B_863	8217
1175	2961	4747	6533	784CIP2B_864	8223

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1176	2962	4748	6534	784CIP2B_865	8224
1177	2963	4749	6535	784CIP2B_866	8226
1178	2964	4750	6536	784CIP2B_867	8227
1179	2965	4751	6537	784CIP2B_868	8229
1180	2966	4752	6538	784CIP2B_869	8232
1181	2967	4753	6539	784CIP2B_870	8236
1182	2968	4754	6540	784CIP2B_871	8239
1183	2969	4755	6541	784CIP2B_872	8244
1184	2970	4756	6542	784CIP2B_873	8245
1185	2971	4757	6543	784CIP2B_874	8248
1186	2972	4758	6544	784CIP2B_875	8251
1187	2973	4759	6545	784CIP2B_876	8253
1188	2974	4760	6546	784CIP2B_877	8260
1189	2975	4761	6547	784CIP2B_878	8262
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1191	2977	4763	6549	784CIP2B_880	8270
1192	2978	4764	6550	784CIP2B_881	8272
1193	2979	4765	6551	784CIP2B_882	8274
1194	2980	4766	6552	784CIP2B_883	8274
1195	2981	4767	6553	784CIP2B_884	8275
1196	2982	4768	6554	784CIP2B_885	8277
1197	2983	4769	6555	784CIP2B_886	8281
1198	2984	4770	6556	784CIP2B_887	8283
1199	2985	4771	6557	784CIP2B_888	8289
1200	2986	4772	6558	784CIP2B_889	8295
1201	2987	4773	6559	784CIP2B_890	8300
1202	2988	4774	6560	784CIP2B_891	8303
1203	2989	4775	6561	784CIP2B_892	8304
1204	2990	4776	6562	784CIP2B_893	8305
1205	2991	4777	6563	784CIP2B_894	8309
1206	2992	4778	6564	784CIP2B_895	8318
1207	2993	4779	6565	784CIP2B_896	8319
1208	2994	4780	6566	784CIP2B_897	8321
1209	2995	4781	6567	784CIP2B_898	8322
1210	2996	4782	6568	784CIP2B_899	8323
1211	2997	4783	6569	784CIP2B_900	8325
1212	2998	4784	6570	784CIP2B_901	8331
1213	2999	4785	6571	784CIP2B_902	8332
1214	3000	4786	6572	784CIP2B_903	8333
1215	3001	4787	6573	784CIP2B_904	8335
1216	3002	4788	6574	784CIP2B_905	8336
1217	3003	4789	6575	784CIP2B_906	8337
1218	3004	4790	6576	784CIP2B_907	8340
1219	3005	4791	6577	784CIP2B_908	8343
1220	3006	4792	6578	784CIP2B_909	8347
1221	3007	4793	6579	784CIP2B_910	8349
1222	3008	4794	6580	784CIP2B_911	8351
1223	3009	4795	6581	784CIP2B_912	8353
1224	3010	4796	6582	784CIP2B_913	8355
1225	3011	4797	6583	784CIP2B_914	8361
1226	3012	4798	6584	784CIP2B_915	8365
1227	3013	4799	6585	784CIP2B_916	8367
1228	3014	4800	6586	784CIP2B_917	8369
1229	3015	4801	6587	784CIP2B_919	8375
1230	3016	4802	6588	784CIP2B_920	8387
1231	3017	4803	6589	784CIP2B_921	8391
1232	3018	4804	6590	784CIP2B_922	8393
1233	3019	4805	6591	784CIP2B_923	8393
1234	3020	4806	6592	784CIP2B_924	8394
1235	3021	4807	6593	784CIP2B_925	8395
1236	3022	4808	6594	784CIP2B_926	8396
1237	3023	4809	6595	784CIP2B_927	8398

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1238	3024	4810	6596	784CIP2B_928	8402
1239	3025	4811	6597	784CIP2B_929	8402
1240	3026	4812	6598	784CIP2B_930	8405
1241	3027	4813	6599	784CIP2B_931	8406
1242	3028	4814	6600	784CIP2B_932	8409
1243	3029	4815	6601	784CIP2B_933	8410
1244	3030	4816	6602	784CIP2B_934	8414
1245	3031	4817	6603	784CIP2B_935	8415
1246	3032	4818	6604	784CIP2B_936	8419
1247	3033	4819	6605	784CIP2B_937	8426
1248	3034	4820	6606	784CIP2B_938	8430
1249	3035	4821	6607	784CIP2B_939	8431
1250	3036	4822	6608	784CIP2B_940	8432
1251	3037	4823	6609	784CIP2B_941	8433
1252	3038	4824	6610	784CIP2B_942	8434
1253	3039	4825	6611	784CIP2B_943	8438
1254	3040	4826	6612	784CIP2B_944	8439
1255	3041	4827	6613	784CIP2B_945	8441
1256	3042	4828	6614	784CIP2B_946	8450
1257	3043	4829	6615	784CIP2B_947	8451
1258	3044	4830	6616	784CIP2B_948	8452
1259	3045	4831	6617	784CIP2B_949	8460
1260	3046	4832	6618	784CIP2B_950	8461
1261	3047	4833	6619	784CIP2B_951	8462
1262	3048	4834	6620	784CIP2B_952	8464
1263	3049	4835	6621	784CIP2B_953	8465
1264	3050	4836	6622	784CIP2B_954	8467
1265	3051	4837	6623	784CIP2B_955	8470
1266	3052	4838	6624	784CIP2B_956	8471
1267	3053	4839	6625	784CIP2B_957	8473
1268	3054	4840	6626	784CIP2B_958	8474
1269	3055	4841	6627	784CIP2B_959	8475
1270	3056	4842	6628	784CIP2B_960	8476
1271	3057	4843	6629	784CIP2B_961	8480
1272	3058	4844	6630	784CIP2B_962	8482
1273	3059	4845	6631	784CIP2B_963	8482
1274	3060	4846	6632	784CIP2B_964	8486
1275	3061	4847	6633	784CIP2B_965	8488
1276	3062	4848	6634	784CIP2B_966	8492
1277	3063	4849	6635	784CIP2B_967	8494
1278	3064	4850	6636	784CIP2B_968	8496
1279	3065	4851	6637	784CIP2B_969	8497
1280	3066	4852	6638	784CIP2B_970	8499
1281	3067	4853	6639	784CIP2B_971	8513
1282	3068	4854	6640	784CIP2B_972	8522
1283	3069	4855	6641	784CIP2B_973	8526
1284	3070	4856	6642	784CIP2B_974	8531
1285	3071	4857	6643	784CIP2B_975	8533
1286	3072	4858	6644	784CIP2B_976	8542
1287	3073	4859	6645	784CIP2B_977	8544
1288	3074	4860	6646	784CIP2B_978	8565
1289	3075	4861	6647	784CIP2B_979	8565
1290	3076	4862	6648	784CIP2B_980	8572
1291	3077	4863	6649	784CIP2B_981	8576
1292	3078	4864	6650	784CIP2B_982	8578
1293	3079	4865	6651	784CIP2B_983	8584
1294	3080	4866	6652	784CIP2B_984	8598
1295	3081	4867	6653	784CIP2B_985	8602
1296	3082	4868	6654	784CIP2B_986	8604
1297	3083	4869	6655	784CIP2B_987	8609
1298	3084	4870	6656	784CIP2B_988	8612
1299	3085	4871	6657	784CIP2B_989	8637

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1300	3086	4872	6658	784CIP2B_990	8640
1301	3087	4873	6659	784CIP2B_991	8643
1302	3088	4874	6660	784CIP2B_992	8645
1303	3089	4875	6661	784CIP2B_993	8650
1304	3090	4876	6662	784CIP2B_994	8651
1305	3091	4877	6663	784CIP2B_995	8654
1306	3092	4878	6664	784CIP2B_996	8655
1307	3093	4879	6665	784CIP2B_997	8657
1308	3094	4880	6666	784CIP2B_998	8665
1309	3095	4881	6667	784CIP2B_999	8668
1310	3096	4882	6668	784CIP2B_1000	8671
1311	3097	4883	6669	784CIP2B_1001	8672
1312	3098	4884	6670	784CIP2B_1002	8692
1313	3099	4885	6671	784CIP2B_1003	8706
1314	3100	4886	6672	784CIP2B_1004	8716
1315	3101	4887	6673	784CIP2B_1005	8719
1316	3102	4888	6674	784CIP2B_1006	8743
1317	3103	4889	6675	784CIP2B_1007	8764
1318	3104	4890	6676	784CIP2B_1008	8764
1319	3105	4891	6677	784CIP2B_1009	8764
1320	3106	4892	6678	784CIP2B_1010	8774
1321	3107	4893	6679	784CIP2B_1011	8782
1322	3108	4894	6680	784CIP2B_1012	8796
1323	3109	4895	6681	784CIP2B_1013	8827
1324	3110	4896	6682	784CIP2B_1014	8842
1325	3111	4897	6683	784CIP2B_1015	8842
1326	3112	4898	6684	784CIP2B_1016	8858
1327	3113	4899	6685	784CIP2B_1017	8871
1328	3114	4900	6686	784CIP2B_1018	8921
1329	3115	4901	6687	784CIP2B_1019	8927
1330	3116	4902	6688	784CIP2B_1020	8942
1331	3117	4903	6689	784CIP2B_1021	8994
1332	3118	4904	6690	784CIP2B_1022	9023
1333	3119	4905	6691	784CIP2B_1023	9028
1334	3120	4906	6692	784CIP2B_1024	9058
1335	3121	4907	6693	784CIP2B_1025	9058
1336	3122	4908	6694	784CIP2B_1026	9079
1337	3123	4909	6695	784CIP2B_1027	9079
1338	3124	4910	6696	784CIP2B_1028	9082
1339	3125	4911	6697	784CIP2B_1029	9084
1340	3126	4912	6698	784CIP2B_1030	9093
1341	3127	4913	6699	784CIP2B_1031	9101
1342	3128	4914	6700	784CIP2B_1032	9103
1343	3129	4915	6701	784CIP2B_1033	9105
1344	3130	4916	6702	784CIP2B_1034	9151
1345	3131	4917	6703	784CIP2B_1035	9161
1346	3132	4918	6704	784CIP2B_1036	9172
1347	3133	4919	6705	784CIP2B_1037	9174
1348	3134	4920	6706	784CIP2B_1038	9204
1349	3135	4921	6707	784CIP2B_1039	9234
1350	3136	4922	6708	784CIP2B_1040	9235
1351	3137	4923	6709	784CIP2B_1041	9239
1352	3138	4924	6710	784CIP2B_1042	9256
1353	3139	4925	6711	784CIP2B_1043	9276
1354	3140	4926	6712	784CIP2B_1044	9345
1355	3141	4927	6713	784CIP2B_1045	9379
1356	3142	4928	6714	784CIP2B_1046	9435
1357	3143	4929	6715	784CIP2B_1047	9437
1358	3144	4930	6716	784CIP2B_1048	9469
1359	3145	4931	6717	784CIP2B_1049	9500
1360	3146	4932	6718	784CIP2B_1050	9502
1361	3147	4933	6719	784CIP2B_1051	9520

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1362	3148	4934	6720	784CIP2B_1052	9541
1363	3149	4935	6721	784CIP2B_1053	9541
1364	3150	4936	6722	784CIP2B_1054	9548
1365	3151	4937	6723	784CIP2B_1055	9556
1366	3152	4938	6724	784CIP2B_1056	9556
1367	3153	4939	6725	784CIP2B_1057	9575
1368	3154	4940	6726	784CIP2B_1058	9589
1369	3155	4941	6727	784CIP2B_1059	9599
1370	3156	4942	6728	784CIP2B_1060	9602
1371	3157	4943	6729	784CIP2B_1061	9606
1372	3158	4944	6730	784CIP2B_1062	9622
1373	3159	4945	6731	784CIP2B_1063	9623
1374	3160	4946	6732	784CIP2B_1064	9646
1375	3161	4947	6733	784CIP2B_1065	9747
1376	3162	4948	6734	784CIP2B_1066	9773
1377	3163	4949	6735	784CIP2B_1067	9785
1378	3164	4950	6736	784CIP2B_1068	9801
1379	3165	4951	6737	784CIP2B_1069	9811
1380	3166	4952	6738	784CIP2B_1070	9843
1381	3167	4953	6739	784CIP2B_1071	9854
1382	3168	4954	6740	784CIP2B_1072	9854
1383	3169	4955	6741	784CIP2B_1073	9864
1384	3170	4956	6742	784CIP2B_1074	9864
1385	3171	4957	6743	784CIP2B_1075	9871
1386	3172	4958	6744	784CIP2B_1076	9879
1387	3173	4959	6745	784CIP2B_1077	9881
1388	3174	4960	6746	784CIP2B_1078	9885
1389	3175	4961	6747	784CIP2B_1079	9901
1390	3176	4962	6748	784CIP2B_1080	9912
1391	3177	4963	6749	784CIP2B_1081	9916
1392	3178	4964	6750	784CIP2B_1082	9921
1393	3179	4965	6751	784CIP2B_1083	9925
1394	3180	4966	6752	784CIP2B_1084	9930
1395	3181	4967	6753	784CIP2B_1085	9949
1396	3182	4968	6754	784CIP2B_1086	9951
1397	3183	4969	6755	784CIP2B_1087	9959
1398	3184	4970	6756	784CIP2B_1088	9973
1399	3185	4971	6757	784CIP2B_1089	9982
1400	3186	4972	6758	784CIP2B_1090	9994
1401	3187	4973	6759	784CIP2B_1091	10021
1402	3188	4974	6760	784CIP2B_1092	10041
1403	3189	4975	6761	784CIP2B_1094	10067
1404	3190	4976	6762	784CIP2B_1095	10073
1405	3191	4977	6763	784CIP2B_1096	10112
1406	3192	4978	6764	784CIP2B_1097	10117
1407	3193	4979	6765	784CIP2B_1098	10132
1408	3194	4980	6766	784CIP2B_1099	10169
1409	3195	4981	6767	784CIP2B_1100	10217
1410	3196	4982	6768	784CIP2B_1101	10226
1411	3197	4983	6769	784CIP2B_1102	10232
1412	3198	4984	6770	784CIP2B_1103	10237
1413	3199	4985	6771	784CIP2B_1104	10279
1414	3200	4986	6772	784CIP2C_1	33
1415	3201	4987	6773	784CIP2C_2	271
1416	3202	4988	6774	784CIP2C_3	848
1417	3203	4989	6775	784CIP2C_4	849
1418	3204	4990	6776	784CIP2C_5	864
1419	3205	4991	6777	784CIP2C_6	953
1420	3206	4992	6778	784CIP2C_7	980
1421	3207	4993	6779	784CIP2C_8	1595
1422	3208	4994	6780	784CIP2C_9	1697
1423	3209	4995	6781	784CIP2C_10	1744

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1424	3210	4996	6782	784CIP2C_11	1937
1425	3211	4997	6783	784CIP2C_12	1955
1426	3212	4998	6784	784CIP2C_13	1955
1427	3213	4999	6785	784CIP2C_14	2185
1428	3214	5000	6786	784CIP2C_15	2889
1429	3215	5001	6787	784CIP2C_16	2901
1430	3216	5002	6788	784CIP2C_17	2902
1431	3217	5003	6789	784CIP2C_18	2905
1432	3218	5004	6790	784CIP2C_19	2948
1433	3219	5005	6791	784CIP2C_20	2956
1434	3220	5006	6792	784CIP2C_21	2959
1435	3221	5007	6793	784CIP2C_22	2965
1436	3222	5008	6794	784CIP2C_23	2966
1437	3223	5009	6795	784CIP2C_24	2970
1438	3224	5010	6796	784CIP2C_25	2985
1439	3225	5011	6797	784CIP2C_26	2987
1440	3226	5012	6798	784CIP2C_27	2993
1441	3227	5013	6799	784CIP2C_28	2993
1442	3228	5014	6800	784CIP2C_29	3017
1443	3229	5015	6801	784CIP2C_30	3046
1444	3230	5016	6802	784CIP2C_31	3050
1445	3231	5017	6803	784CIP2C_32	3357
1446	3232	5018	6804	784CIP2C_33	3359
1447	3233	5019	6805	784CIP2C_34	3432
1448	3234	5020	6806	784CIP2C_35	3438
1449	3235	5021	6807	784CIP2C_36	3439
1450	3236	5022	6808	784CIP2C_39	3463
1451	3237	5023	6809	784CIP2C_40	3466
1452	3238	5024	6810	784CIP2C_41	3466
1453	3239	5025	6811	784CIP2C_42	3467
1454	3240	5026	6812	784CIP2C_43	3468
1455	3241	5027	6813	784CIP2C_44	3483
1456	3242	5028	6814	784CIP2C_45	3484
1457	3243	5029	6815	784CIP2C_46	3488
1458	3244	5030	6816	784CIP2C_47	3491
1459	3245	5031	6817	784CIP2C_48	3493
1460	3246	5032	6818	784CIP2C_49	3494
1461	3247	5033	6819	784CIP2C_50	3495
1462	3248	5034	6820	784CIP2C_51	3496
1463	3249	5035	6821	784CIP2C_52	3503
1464	3250	5036	6822	784CIP2C_53	3503
1465	3251	5037	6823	784CIP2C_54	3504
1466	3252	5038	6824	784CIP2C_55	3511
1467	3253	5039	6825	784CIP2C_56	3531
1468	3254	5040	6826	784CIP2C_57	3536
1469	3255	5041	6827	784CIP2C_58	3546
1470	3256	5042	6828	784CIP2C_59	3548
1471	3257	5043	6829	784CIP2C_60	3551
1472	3258	5044	6830	784CIP2C_61	3553
1473	3259	5045	6831	784CIP2C_62	3564
1474	3260	5046	6832	784CIP2C_63	3567
1475	3261	5047	6833	784CIP2C_64	3572
1476	3262	5048	6834	784CIP2C_65	3573
1477	3263	5049	6835	784CIP2C_66	3574
1478	3264	5050	6836	784CIP2C_67	3583
1479	3265	5051	6837	784CIP2C_68	3615
1480	3266	5052	6838	784CIP2C_69	3623
1481	3267	5053	6839	784CIP2C_70	3629
1482	3268	5054	6840	784CIP2C_71	3666
1483	3269	5055	6841	784CIP2C_72	3667
1484	3270	5056	6842	784CIP2C_73	3906
1485	3271	5057	6843	784CIP2C_74	3912

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
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1487	3273	5059	6845	784CIP2C_76	3928
1488	3274	5060	6846	784CIP2C_77	3935
1489	3275	5061	6847	784CIP2C_78	3959
1490	3276	5062	6848	784CIP2C_79	3981
1491	3277	5063	6849	784CIP2C_80	3989
1492	3278	5064	6850	784CIP2C_81	4295
1493	3279	5065	6851	784CIP2C_82	4300
1494	3280	5066	6852	784CIP2C_83	4360
1495	3281	5067	6853	784CIP2C_84	4362
1496	3282	5068	6854	784CIP2C_85	4371
1497	3283	5069	6855	784CIP2C_86	4373
1498	3284	5070	6856	784CIP2C_87	4376
1499	3285	5071	6857	784CIP2C_89	4378
1500	3286	5072	6858	784CIP2C_90	4382
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1505	3291	5077	6863	784CIP2C_95	4430
1506	3292	5078	6864	784CIP2C_96	4435
1507	3293	5079	6865	784CIP2C_97	4436
1508	3294	5080	6866	784CIP2C_98	4439
1509	3295	5081	6867	784CIP2C_99	4440
1510	3296	5082	6868	784CIP2C_100	4441
1511	3297	5083	6869	784CIP2C_101	4442
1512	3298	5084	6870	784CIP2C_102	4455
1513	3299	5085	6871	784CIP2C_103	4462
1514	3300	5086	6872	784CIP2C_104	4466
1515	3301	5087	6873	784CIP2C_105	4469
1516	3302	5088	6874	784CIP2C_106	4477
1517	3303	5089	6875	784CIP2C_107	4481
1518	3304	5090	6876	784CIP2C_108	4483
1519	3305	5091	6877	784CIP2C_109	4484
1520	3306	5092	6878	784CIP2C_110	4486
1521	3307	5093	6879	784CIP2C_111	4490
1522	3308	5094	6880	784CIP2C_112	4499
1523	3309	5095	6881	784CIP2C_113	4503
1524	3310	5096	6882	784CIP2C_114	4506
1525	3311	5097	6883	784CIP2C_115	4509
1526	3312	5098	6884	784CIP2C_116	4514
1527	3313	5099	6885	784CIP2C_117	4516
1528	3314	5100	6886	784CIP2C_118	4522
1529	3315	5101	6887	784CIP2C_119	4525
1530	3316	5102	6888	784CIP2C_120	4527
1531	3317	5103	6889	784CIP2C_121	4528
1532	3318	5104	6890	784CIP2C_122	4529
1533	3319	5105	6891	784CIP2C_123	4532
1534	3320	5106	6892	784CIP2C_124	4537
1535	3321	5107	6893	784CIP2C_125	4538
1536	3322	5108	6894	784CIP2C_126	4551
1537	3323	5109	6895	784CIP2C_127	4552
1538	3324	5110	6896	784CIP2C_128	4559
1539	3325	5111	6897	784CIP2C_129	4567
1540	3326	5112	6898	784CIP2C_130	4568
1541	3327	5113	6899	784CIP2C_132	4585
1542	3328	5114	6900	784CIP2C_133	4592
1543	3329	5115	6901	784CIP2C_134	4609
1544	3330	5116	6902	784CIP2C_135	4616
1545	3331	5117	6903	784CIP2C_136	4617
1546	3332	5118	6904	784CIP2C_137	4618
1547	3333	5119	6905	784CIP2C_138	4620

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1548	3334	5120	6906	784CIP2C_139	4624
1549	3335	5121	6907	784CIP2C_140	4632
1550	3336	5122	6908	784CIP2C_141	4634
1551	3337	5123	6909	784CIP2C_142	4638
1552	3338	5124	6910	784CIP2C_143	4639
1553	3339	5125	6911	784CIP2C_144	4643
1554	3340	5126	6912	784CIP2C_145	4644
1555	3341	5127	6913	784CIP2C_146	4655
1556	3342	5128	6914	784CIP2C_147	4668
1557	3343	5129	6915	784CIP2C_148	4677
1558	3344	5130	6916	784CIP2C_149	4677
1559	3345	5131	6917	784CIP2C_150	4677
1560	3346	5132	6918	784CIP2C_152	4682
1561	3347	5133	6919	784CIP2C_153	4690
1562	3348	5134	6920	784CIP2C_154	4691
1563	3349	5135	6921	784CIP2C_155	4727
1564	3350	5136	6922	784CIP2C_156	4730
1565	3351	5137	6923	784CIP2C_157	4734
1566	3352	5138	6924	784CIP2C_158	4757
1567	3353	5139	6925	784CIP2C_159	4764
1568	3354	5140	6926	784CIP2C_160	4786
1569	3355	5141	6927	784CIP2C_161	4793
1570	3356	5142	6928	784CIP2C_162	4825
1571	3357	5143	6929	784CIP2C_163	4826
1572	3358	5144	6930	784CIP2C_164	4850
1573	3359	5145	6931	784CIP2C_165	4853
1574	3360	5146	6932	784CIP2C_166	4855
1575	3361	5147	6933	784CIP2C_167	4856
1576	3362	5148	6934	784CIP2C_168	4867
1577	3363	5149	6935	784CIP2C_169	4869
1578	3364	5150	6936	784CIP2C_170	4878
1579	3365	5151	6937	784CIP2C_171	4880
1580	3366	5152	6938	784CIP2C_172	4942
1581	3367	5153	6939	784CIP2C_173	4945
1582	3368	5154	6940	784CIP2C_174	4950
1583	3369	5155	6941	784CIP2C_175	4952
1584	3370	5156	6942	784CIP2C_176	4954
1585	3371	5157	6943	784CIP2C_177	4958
1586	3372	5158	6944	784CIP2C_178	4961
1587	3373	5159	6945	784CIP2C_179	5590
1588	3374	5160	6946	784CIP2C_180	5599
1589	3375	5161	6947	784CIP2C_181	5692
1590	3376	5162	6948	784CIP2C_182	5732
1591	3377	5163	6949	784CIP2C_183	5765
1592	3378	5164	6950	784CIP2C_184	5771
1593	3379	5165	6951	784CIP2C_185	5774
1594	3380	5166	6952	784CIP2C_186	5793
1595	3381	5167	6953	784CIP2C_187	5806
1596	3382	5168	6954	784CIP2C_188	5852
1597	3383	5169	6955	784CIP2C_189	5892
1598	3384	5170	6956	784CIP2C_190	6057
1599	3385	5171	6957	784CIP2C_191	6061
1600	3386	5172	6958	784CIP2C_192	6109
1601	3387	5173	6959	784CIP2C_193	6160
1602	3388	5174	6960	784CIP2C_194	6297
1603	3389	5175	6961	784CIP2C_195	6398
1604	3390	5176	6962	784CIP2C_196	6398
1605	3391	5177	6963	784CIP2C_197	6415
1606	3392	5178	6964	784CIP2C_198	6448
1607	3393	5179	6965	784CIP2C_199	6469
1608	3394	5180	6966	784CIP2C_200	6476
1609	3395	5181	6967	784CIP2C_201	6561

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1610	3396	5182	6968	784CIP2C_202	6574
1611	3397	5183	6969	784CIP2C_203	6578
1612	3398	5184	6970	784CIP2C_204	6662
1613	3399	5185	6971	784CIP2C_205	6672
1614	3400	5186	6972	784CIP2C_206	6691
1615	3401	5187	6973	784CIP2C_207	6695
1616	3402	5188	6974	784CIP2C_208	6746
1617	3403	5189	6975	784CIP2C_209	6898
1618	3404	5190	6976	784CIP2C_210	6938
1619	3405	5191	6977	784CIP2C_211	6943
1620	3406	5192	6978	784CIP2C_212	7110
1621	3407	5193	6979	784CIP2C_213	7200
1622	3408	5194	6980	784CIP2C_214	7212
1623	3409	5195	6981	784CIP2C_215	7218
1624	3410	5196	6982	784CIP2C_216	7249
1625	3411	5197	6983	784CIP2C_217	7500
1626	3412	5198	6984	784CIP2C_218	7509
1627	3413	5199	6985	784CIP2C_219	7523
1628	3414	5200	6986	784CIP2C_220	7544
1629	3415	5201	6987	784CIP2C_221	7564
1630	3416	5202	6988	784CIP2C_222	7568
1631	3417	5203	6989	784CIP2C_223	7631
1632	3418	5204	6990	784CIP2C_224	7813
1633	3419	5205	6991	784CIP2C_225	7831
1634	3420	5206	6992	784CIP2C_226	7843
1635	3421	5207	6993	784CIP2C_227	7907
1636	3422	5208	6994	784CIP2C_228	7943
1637	3423	5209	6995	784CIP2C_229	8175
1638	3424	5210	6996	784CIP2C_230	8216
1639	3425	5211	6997	784CIP2C_231	8225
1640	3426	5212	6998	784CIP2C_232	8271
1641	3427	5213	6999	784CIP2C_233	8397
1642	3428	5214	7000	784CIP2C_234	8466
1643	3429	5215	7001	784CIP2C_235	8503
1644	3430	5216	7002	784CIP2C_236	8953
1645	3431	5217	7003	784CIP2C_237	9106
1646	3432	5218	7004	784CIP2C_238	9139
1647	3433	5219	7005	784CIP2C_239	9555
1648	3434	5220	7006	784CIP2C_240	9650
1649	3435	5221	7007	784CIP2C_241	9889
1650	3436	5222	7008	784CIP2C_242	9933
1651	3437	5223	7009	784CIP2C_243	9953
1652	3438	5224	7010	784CIP2C_244	9981
1653	3439	5225	7011	784CIP2D_1	746
1654	3440	5226	7012	784CIP2D_2	3558
1655	3441	5227	7013	784CIP2D_3	3558
1656	3442	5228	7014	784CIP2D_4	3633
1657	3443	5229	7015	784CIP2D_5	3658
1658	3444	5230	7016	784CIP2D_6	3732
1659	3445	5231	7017	784CIP2D_7	4004
1660	3446	5232	7018	784CIP2D_8	4700
1661	3447	5233	7019	784CIP2D_9	4703
1662	3448	5234	7020	784CIP2D_10	4774
1663	3449	5235	7021	784CIP2D_11	4894
1664	3450	5236	7022	784CIP2D_12	4918
1665	3451	5237	7023	784CIP2D_13	5159
1666	3452	5238	7024	784CIP2D_14	7443
1667	3453	5239	7025	784CIP2D_15	8673
1668	3454	5240	7026	784CIP2D_16	8679
1669	3455	5241	7027	784CIP2D_17	8727
1670	3456	5242	7028	784CIP2D_18	8734
1671	3457	5243	7029	784CIP2D_19	8756

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1672	3458	5244	7030	784CIP2D_20	8818
1673	3459	5245	7031	784CIP2D_21	8844
1674	3460	5246	7032	784CIP2D_22	8846
1675	3461	5247	7033	784CIP2D_23	8912
1676	3462	5248	7034	784CIP2D_24	8918
1677	3463	5249	7035	784CIP2D_25	8918
1678	3464	5250	7036	784CIP2D_26	8941
1679	3465	5251	7037	784CIP2D_27	8941
1680	3466	5252	7038	784CIP2D_28	8951
1681	3467	5253	7039	784CIP2D_29	8951
1682	3468	5254	7040	784CIP2D_30	9007
1683	3469	5255	7041	784CIP2D_31	9012
1684	3470	5256	7042	784CIP2D_32	9013
1685	3471	5257	7043	784CIP2D_33	9025
1686	3472	5258	7044	784CIP2D_34	9053
1687	3473	5259	7045	784CIP2D_35	9054
1688	3474	5260	7046	784CIP2D_36	9054
1689	3475	5261	7047	784CIP2D_37	9113
1690	3476	5262	7048	784CIP2D_38	9134
1691	3477	5263	7049	784CIP2D_39	9152
1692	3478	5264	7050	784CIP2D_40	9152
1693	3479	5265	7051	784CIP2D_41	9211
1694	3480	5266	7052	784CIP2D_42	9223
1695	3481	5267	7053	784CIP2D_43	9223
1696	3482	5268	7054	784CIP2D_44	9231
1697	3483	5269	7055	784CIP2D_45	9236
1698	3484	5270	7056	784CIP2D_46	9236
1699	3485	5271	7057	784CIP2D_47	9303
1700	3486	5272	7058	784CIP2D_48	9309
1701	3487	5273	7059	784CIP2D_49	9314
1702	3488	5274	7060	784CIP2D_50	9326
1703	3489	5275	7061	784CIP2D_51	9339
1704	3490	5276	7062	784CIP2D_52	9348
1705	3491	5277	7063	784CIP2D_53	9376
1706	3492	5278	7064	784CIP2D_54	9382
1707	3493	5279	7065	784CIP2D_55	9407
1708	3494	5280	7066	784CIP2D_56	9414
1709	3495	5281	7067	784CIP2D_57	9439
1710	3496	5282	7068	784CIP2D_58	9485
1711	3497	5283	7069	784CIP2D_59	9493
1712	3498	5284	7070	784CIP2D_60	9501
1713	3499	5285	7071	784CIP2D_61	9526
1714	3500	5286	7072	784CIP2D_62	9526
1715	3501	5287	7073	784CIP2D_63	9551
1716	3502	5288	7074	784CIP2D_64	9557
1717	3503	5289	7075	784CIP2D_65	9568
1718	3504	5290	7076	784CIP2D_66	9588
1719	3505	5291	7077	784CIP2D_67	9597
1720	3506	5292	7078	784CIP2D_68	9615
1721	3507	5293	7079	784CIP2D_69	9628
1722	3508	5294	7080	784CIP2D_70	9649
1723	3509	5295	7081	784CIP2D_71	9652
1724	3510	5296	7082	784CIP2D_72	9660
1725	3511	5297	7083	784CIP2D_73	9662
1726	3512	5298	7084	784CIP2D_74	9725
1727	3513	5299	7085	784CIP2D_75	9746
1728	3514	5300	7086	784CIP2D_76	9777
1729	3515	5301	7087	784CIP2D_77	9787
1730	3516	5302	7088	784CIP2D_78	9790
1731	3517	5303	7089	784CIP2D_79	9842
1732	3518	5304	7090	784CIP2D_80	9842
1733	3519	5305	7091	784CIP2D_81	9848

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1734	3520	5306	7092	784CIP2D_82	9867
1735	3521	5307	7093	784CIP2D_83	10010
1736	3522	5308	7094	784CIP2D_84	10011
1737	3523	5309	7095	784CIP2D_85	10052
1738	3524	5310	7096	784CIP2D_86	10057
1739	3525	5311	7097	784CIP2D_87	10085
1740	3526	5312	7098	784CIP2D_89	10139
1741	3527	5313	7099	784CIP2D_90	10142
1742	3528	5314	7100	784CIP2D_92	10165
1743	3529	5315	7101	784CIP2D_93	10173
1744	3530	5316	7102	784CIP2D_94	10173
1745	3531	5317	7103	784CIP2D_95	10273
1746	3532	5318	7104	784CIP2E_1	3121
1747	3533	5319	7105	784CIP2E_2	3628
1748	3534	5320	7106	784CIP2E_4	3673
1749	3535	5321	7107	784CIP2E_5	4018
1750	3536	5322	7108	784CIP2E_6	4467
1751	3537	5323	7109	784CIP2E_7	4865
1752	3538	5324	7110	784CIP2E_8	4916
1753	3539	5325	7111	784CIP2E_9	4923
1754	3540	5326	7112	784CIP2E_10	4926
1755	3541	5327	7113	784CIP2E_11	4962
1756	3542	5328	7114	784CIP2E_12	4963
1757	3543	5329	7115	784CIP2E_13	4964
1758	3544	5330	7116	784CIP2E_14	4988
1759	3545	5331	7117	784CIP2E_15	5835
1760	3546	5332	7118	784CIP2E_16	7682
1761	3547	5333	7119	784CIP2E_17	7682
1762	3548	5334	7120	784CIP2E_18	7699
1763	3549	5335	7121	784CIP2E_19	7707
1764	3550	5336	7122	784CIP2E_20	7707
1765	3551	5337	7123	784CIP2E_21	7752
1766	3552	5338	7124	784CIP2E_22	8357
1767	3553	5339	7125	784CIP2E_23	9065
1768	3554	5340	7126	784CIP2E_24	9324
1769	3555	5341	7127	784CIP2F_1	2976
1770	3556	5342	7128	784CIP2F_2	3559
1771	3557	5343	7129	784CIP2F_3	4021
1772	3558	5344	7130	784CIP2F_4	4474
1773	3559	5345	7131	784CIP2F_5	4566
1774	3560	5346	7132	784CIP2F_6	4705
1775	3561	5347	7133	784CIP2F_7	4707
1776	3562	5348	7134	784CIP2F_8	4712
1777	3563	5349	7135	784CIP2F_9	5008
1778	3564	5350	7136	784CIP2F_10	5009
1779	3565	5351	7137	784CIP2F_11	5015
1780	3566	5352	7138	784CIP2F_12	5015
1781	3567	5353	7139	784CIP2F_13	7724
1782	3568	5354	7140	784CIP2F_14	7725
1783	3569	5355	7141	784CIP2F_15	8828
1784	3570	5356	7142	784CIP2F_16	8830
1785	3571	5357	7143	784CIP2F_17	9739
1786	3572	5358	7144	784CIP2F_18	9896

TABLE 7

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine; M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPG ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW KITQF
5360	2	1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL GTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS SSKELWYMPEHYIRQGKLSIKTDVYSFGIVIMEVLTGCRVVLDD PKHIQLRDLLREIMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC SQSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSQD LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
5362	2	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQKA NNLKTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL FPSPADSGTNSVPSQLENNTNHYSSQIEGNTNSSFLKGGNGENA VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSPLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISRDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFFTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAKVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKFPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND NSRTTATVSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE KAEPASAAEISSVRKEETAVAIQTIEEHPASFDWSSFKPMGFE VSFLKFLERSAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV TSGNHVCPCKESETPVQFANPSQLQCSDNVKIVLDKNLKDCTEL

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			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP \LEGRQKTGLDSP\TGIDPS\DITA\NSFT\VHW\IAPRA/TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKNLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS

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			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQFNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN ITIYAVEENQESTPVVIQQEITGTPRSDTVPSPRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI TGYRIR\HHPEHP\SGRPREDR\VPHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAPTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5365	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNMI RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR

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			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV SGPRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDFTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTP\AEN TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLRVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SND APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTA=PAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5366	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDMGHNMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV SGFRVEYELSERGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDPS\DITA\NSFT\VHN\IAPRA/TPI TGYRIR\HHPRHP\SGRPREDR\VPHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5367	235	3591	KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKYLIIHVLRL ILELWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKEMRHHLQIM EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQPGEKRLV KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEIANYPIYKI LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG KGYPSAVPKDKDRQCFKLRQGIDKKIVIYVQQTTNKELAIERCP GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDILYEVVCLBS ESERKRRKTTASPSVRLPQSGSQSSVIPSPPRDDEBEDNDEPLL SGSGDVSKECAEKILETNGELLSKWHLNLNVRPKQLSSLVRNGV PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPQDSAITRDIN

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			RTFPAHDYFKDTGGDGQDSLYKICKAYSVYDEEIGYCQGQSFLA AVLLLHMPEEQAFSVLVKIMFDYGLRELFKQNFEDLHCKFYQLE RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVFH IIDLLLCEGISVIFNVALGLLKTSKDDLLJ.TDFEGALKFFRVQL PKRYRSEENAKKLMELACNMKISQKKLKKYEKEYHTMREQQAQQ EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD NAEEKADALNK3LLMTKQKLIDAEEEKRRLEEESAHLKKMCRRE LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR QKVDDCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNQL REMELELAQTKL\QLVEASCKIQD\LEHPF*GLPFNE\VQAA\K KTWFNRTLSSIKTATGVQGKETC
5368	573	2014	GAAAGAADPRRGSLGGRTMLDFAIFAVTFLLALVGAVLYLYPAS RQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVS FWFGRRLVVSLGTVDVLKQHINPNKTLD/LF*NHAEVIIKVSIW WWQCE*KP\QRKKLYENGVTDSLKSNFALLLKLPEELLDKNLSY PETQH\VPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG TVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERK GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW AIWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVLC ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREEAWITVSKRY
5369	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED CHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSPS RCLKADVLG/VWRRDQRPERRE\L*IFWGGEDP\VLLTLFTMTY QKKKMECGRMDFPPMNAVLCFSKAVHNLLERCLMNRNFVRIGKWF VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINQHQPVY LLSREHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR MIYPACPVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA MSSVTLTPPTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGGLCEEATA AKVASWDFVEATQRTNCSCLRHKNLKSRNAGQQGQAPSLGQQQQ ILPKHKTNKKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSERRAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGPCSPKPSEIKDFSYVYKPRNCQILVGCSMPAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ

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			TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAF TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV QMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL AFNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP GSHYPHGGDAGKGQSTDRLLSTEPHEEVPNILQQPLALGYFVST AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIH FVVLNQLYNFIMNML
5370	1226	716	RWSRKLELRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDAIDR AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKQS SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMKPMLKKLRI/F LQELGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE ELIKLIEQFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT AAPNVFHNPVEKNKQMVRILQESYLDVGGSEANMKVWLLKLLSQ NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM QGLLREGISIAQIRETPMVLELTPQIVQYRIRKLNSSGYRIKDG HLANLNGSKKEFEANPGKIQAKKVRPLFNPVAPLNVEE
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGRGGME PLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD HRDAGDLWFPG\DLRASRM*MWSTASPGASWKEKSPSHPLPSFS SWPASFSSRF*QPAPSGLQPCMDRSQGHIHPVNWTVAMTQGISS KLCQG
5373	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKQWC ANFKKRAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ \QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5374	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP

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			TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDPSGKAKPS PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SRMKHN LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ \QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS DRKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5375	2907	1116	HIFLAEEKPMLERRCRGPLAMGPAQPRLLSGPSQESPQTLGKES RGLRQQGTSVA\QSGAQAPGRAHRCAHCRRHFPGWVA\LWLHTR RCQA/RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH LCGQSFRGWVALVLHLRAHSAAKAGPPACPKMARDAFWRRKAAS SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV SRRP*ERGPPAKVFWGPRPRGPPTGDTPPGPGGDAVDRPF\QCA CCGKRFRHK\PNLIRSHAACTSGERPHQ/CSRECG\KRFTNKPY LTS\HRRITHTARQPYPCKECGRRFRHKPNLLSHSKIHKRSEGS AQAAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP QDPIRAPPSLYSCDDCGRSFRLERFLRAHQRQHTGERPFTCAEC GKNFGKKTHLVAHSRVHSGERPFRLARKCGRRFLPRASQSGGRN SAEPNAPRPGPFVCPDCGKAFRHKPYLAAHRPIATPAEKPYVCP DCRKAFSQKSNL\VSHRRIHTGERPYACPDCDRSFSQKSNLITH RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
5376	4504	591	VSTFSLCLMPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSARAS ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKWVGVILDEAKG KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKER VDELTTDLEILKAEIEEKGSDGAASSYQLKQLREQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDRLQENARETELELRRQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAPLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS
5377	762	1106	DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WPGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS*WPGYDGWWGGQYIFIFRGMRWEBQP
5378	2009	664	QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR

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			SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VNPIFSEAC
5379	2009	664	QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR SPSPRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VNPIFSEAC
5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM
5381	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGMR SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM.
5382	1536	203	GARGSQQDAPALQEAEVEGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSPSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPDLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFRLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSPANPIQYLLDPHTSKLAPFNEH WRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP

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			PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLPGYPKP ENLLRD
5383	45	5250	VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEELKKLS VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCVQDFSN CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI HLLLCQLRVLEVGALQAVYELERILSRFLEKNADPSASEIREEL EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMESRFN PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVMKDVVL IRKLLALMAQEQKLPREVATPTTDEEKDSLIAIDRSPLSTLPGQ SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIRQILEKKE GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVFATKLTYP QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT QRRAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNRQPTLH RPSIQAHRARILPEEKVLRLHYANCKAYNADPDGDEMNAHFPQS ELGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG CFFTREHYMELVYRGLTDKVGRVKLLSPSILKPFPLWTGKQVVS TLLINIIPEDHIPLNLSGKAKITGKAWVKETPRSVPGFNPDSMC ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV LTCLARLFTAYLQLYRGFTLGVRDILVKPKADVKRQRIIEESTH CGPQAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNMIDLKF KREVNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT MQISCLLGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG RFLTGIKPDREFFFHCMAGREGLVDTAVKTSRSGYLQRCIIKHLE GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPPLA SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHPNTLER RGAPLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMMY ELDEESRRKYQKKAAACPDPSLSVWRPDIYFASVSETFETKVDD YSQEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLREILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRPMET RFFKLLMESIKKKNNKASAFRNVNTRRATQRDLDNAGELGRSRG EQEGDEEEEGHIVDAEAEEGDADASDAKRKEKQEEEVDYESEER ERREGRENDDEDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC LINETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLPELKQPLR
5384	196	886	QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPKIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD
5385	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVESHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT
5386	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT
5387	2	2117	FVVAASGGCNFVLGERRAGSLLSASYGTFAMPGMVLPGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT

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			SVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTYPSDTDLVPSD IAAGLALLHQQQDNIRNNQEPAQVVCHAPGSSQEADLDAELKNC HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGAA ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAQGVSSV DVA
5388	1569	753	TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRRAACQAERPAARS KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK ILEHLQTKN
5389	1569	753	TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRRAACQAERPAARS KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK ILEHLQTKN
5390	217	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIQGEEI SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS TSLCWNDLSWFQSITRLPIILKGILTKEDAKLAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVAEINRNLVQFSRL
5391	1	1292	VKKAAGRERGPPTAGGQRCEEAPGTVMERRLGVRANVKENRGSF QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEEGEEVFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS
5392	1	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTERQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP
5393	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG

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			\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP RAPTDDDKNIYLTLPPNDHVNSNN
5394	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG \NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP RAPTDDDKNIYLTLPPNDHVNSNN
5395	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME ANGVDGDGLNKPAKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5396	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG RKTLPLTTAPRAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME ANGVDGDGLNKPAKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5397	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL

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			PQQSYNFDPDTCDRSVDPFKTSSKTPSSPSKSPASFEIPASAME ANGVDGDGLNKPAKKKTPLKTDTPRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKPSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSPEETE ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5398	56	5426	SGEVCRMESNFNQEGVPRPSYVFSADPIARPSEINFDGIKLDLS HEFSLVAPNTEANSFESKDYLQVCLRIRPFTQSEKELESEGCVH ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKFSFPPGPLGPAT TQKEPFQGCIMHP\VKDLLKGQSRLIFTYGLTNSGKTYTFQGTE ENIRILPRTLNVLFDSLQERLYTKMNLKPHRSRRYLRLSSEQEK EEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESIK DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKRK MLRLSQDVKGYSFIKDLQWIQVSDSKEAYRLLKLGIKHQSVAFT KLNNASSRSHSIFTVKILQIEDSEMSRVIRVSELSLCDLAGSER TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKFQQHVP FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS AIAQKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVKR ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLLDEDLDK TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE EVTQEFTQYWAQREADFKETLLQERELLEENAERRLAIFKDLVG KCDTREEAAKDICATKVETEEATACLELKFNQIKAELAKTKGEL IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIIDQ KEDTINEFQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEV PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK SEEVRPNIAEIEDIRVLQENNEGLRAFLLTIENELKNEKEEKAE LNKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK SKNQEQEEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTL DSVSQISNIDLLNLRDLSNGSEEDNLPNTQLDLLGNDYLVSKQV KEYRIQEPNRENSFHSSIEAIWEECKEIVKASSKKSHQIEELEQ QIEKLQAEVKGYKDENNRLKEKEHKNQDDLLKRKETLIQQLKEE LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE TQKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNT KDLNVKELKLKEEITQLTNNLQDMKHLLQLKEEEEETNRQETEK LKEELSASSARTQN\LNADLQRKEEDYADLKEKLTDAKKQIKQV QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK EQLINQKVEEAIQQYERACKDLNVKEKIIEDMRMTLEEQEQTQV EQDQVL\EAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE NNTDVLGKLTNLQDELQESEQKYNADRKKWLEEKMMLITQAKEA ENIRNKEMKKYAEDREREFKQQNEMEILTAQLTEKDSDLQKWRE ERDQLVAALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV STENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKETYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK
5399	705	230	GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY
5400	931	248	SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVREIIQKQVKVNCTAEVLYPSTGQE TAPEVNFTFEGETGKNPDREDNTFYQRLKSMKEPLEAQNI\PDN

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			FGNVSPEMTLVLHLAWVACGYIIWQNSTEDTWYKMVKIQTVKQV QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS RLPKEVQLE
5401	3	1360	TGWSYGPTTSLAFLAPRDFPPPPKLLIHPQAVVRLSCGAGSMGS QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME KWAPRQDDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD SKKLPGLGDPDIDWEESVCLNLILQKLDYMVTCAVCTRADGGDI HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\EE\ VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY DNRVSVAARMAQK\MSFGFSKYSNMEP\VR\MKGPQGKGHAEMA VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI LTDILEVRQKPILMT
5402	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS QVAMKQNELLEPNSF
5403	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS QVAMKQNELLEPNSF
5404	187	1111	LPVTLIFAKMKTLQSTLLLLLLVPLIKPAPPTQQDSRIIYDYGT DNFERSIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDEAI TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY LYARFNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL SLVEELSLAENQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK KLNNLTFLYLDHNALESVPLNLPESLRVIHLQFNNIASITDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
5405	2199	1220	QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLESCPSRGQGKPS
5406	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQQNLYRNVMLENY

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			RNLVPLG/YIAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC SHFTQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVDE CKVHRGGYNGFNQCLPATQSKIPLFDKCVKAFHKFSNSNRHKIS HTEKKLFKCKECGKSFCMLSHLAQHKIIHTRVNFCKCEKCGKAF NCPSIITKHKRINTGEKPYTCEECGKVFNWSSRLTTHKKNYTRY KLYKCEECGKAFNKSSILTTHKIIRTGEKPYKCKECAKAFNQSS NLTEHKKIHPGEKPYKCEECGKAFNWPSTLTKHKRIHTGEKPYT CEECGKAFNQFSNLTTHKRIHTA\EKPYKCTECGEAFSRS\SNL TKHKEIHTEKKPYKCEECGKAFKWSSKLTEHKLTHTGEKPYKCE KCGKAFNCPSIITKHNRINTGEKPYTCEECGKVFNWSSRLTTHK KNYTRYKLYKCEECGKAFNKSSILTTHKKIHIEKKFYKCEECGK AFKWSSKLTEHKITHTGEKPYKCEECGKAFNHFSILTKHKRIHT GEKPYKCEECGKAFTQSSNLTTHKKIHTGEKFYKCEECGKAFTQ SSNLTTHKKIHTGGKPYKCEECGKAFNQFSTLTKHKIIHTEKKP YKCEECGKAFKWSSTLTKHKIIHTGEKPYKCEECG\KAFKLSST LSTHKIIHTGEKPYKCEKCGKAFNRPSNLIEHKKI:HTGEQPYKC EECGKAFNYSSHLNTHKRIHTKEQPYKCKECGKAFNQYSNLTTH NKIHTGEKLYKPEDVTVILTTPQTFSNIK
5407	3	659	RPRRRQSSCCTGWLAGWLLRAAPRFCRRTETDMEQGKGLAVLIL AIILLQGTLAQSIKGNHLVKVYDYQEDGSVLLTCDAEAKNITWF KDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVY YRMCQNCIELNAATISGFLFAEIVSIFDLAVGVYFIAGTGMEFR QS\RASDKQTLLP\NDPAPTQPLKDPRKMTQYSHLQGN\QLRRN
5408	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRPLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNFVVPCGTEX NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQPLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ
5409	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRPLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFN NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

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			TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ
5410	2	710	LRFPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY VHQNFSSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLPNG KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC SG\CAKILVGTFAGVW
5411	1302	289	TGPAAAGRRKALGSFGKPSPVTGLRAARRRRTRPSAPAAPSVGC GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLQNHQQPN GGEPFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	QGISNFFHKEANFWFEVSGYLISPLRSPFVDPALEWSLMASPNN KMEGESSRFEIHTPVSDKKKKCSIHKERPQKHSHEIFRDSSLV NEQSQITRRKKRKKDFQHLISSPLKKSRICDETANATSTLKKRK KRRYSALEVDEEAGVTVVLVDKENINNTPKHFRKDVDVVCVDMS IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA HKNKSKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV GLDDETPQLLGPTHKKKSKKKKKKSNHQEFESLAMPEGSQVGS EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKSNHQEF EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK SKKRKLTSVKRARVSGDDFSVPSKNSESTLFDSVEGDGAMMEEG VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSEIRY LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQELK EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDTNEI DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPEIIDYL YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	RFPAGVAPRRAMANVSKKVSWSGRDRDDERAAPLLRRTARPGGG TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG VSAAFGAPVGGVLFSLEEGASFWNQPLTWRIFFASMISTFTLNF VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK

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			SVVSLFHDPPGSYNPLTLGLPTLVYPFLACWTYGLTVSAGVFIP SLLIGAAWGRLFGISLSYLTGAAIWADPGKYALMGAAAQLGGIV RMTLSLTVIMMEATSNVTYGFPIMLVLMTAKIVGDVFIEGLYDM HIQLQSVPFLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV DVLSDTASNHNGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSQDERECTMD LSEFMNPSPYTVPQEASLPRVFKLFRALGLRHLVVVDNRNQVVG LVTRKDLARYRLGKRGLERLSLAQT
5414	2130	390	GVASAWDRALFSPLLSPTSRVFRTSPPRCVSTETGRRDRARVPS QWCSVLQGKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR AGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGCQGPRGTRSP RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINNLNYMDRFTV AGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDRYN RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASY STIAPTLIADLFVADQRSRMLSIFYFAIPVGSGLGYIAGSKVKD MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPL NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLL RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYIF IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD AGSPYLIGLISDRLRRNWPPSFLSRFRALQFSLMLCAPVGALGG AAFLGTAHLH
5415	693	2986	IPPKTKLELQKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEL IISFLRCLPERKQKEHIHIGEMKQTSQMAAENIGSELPPSATRF RLDMLKNKAKRSLTESLESILSRGNKARGLQEHSISVDLDSSLS STLSNTSKEPSVCEKEALPISESSFKLLGSSEDLSSDSESHLPE EPAPLSPQQAFRRRANTLSHFPIECQEPQPARGSPGVSQRKLM RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFL RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPE EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKR LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ GVP\RHHRGEIWKFLAEQFHLKHQFPSKQQPKDVPYKELLKQLT SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE VGYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLRKQYRPDM IILQIQMYQLSRLLHDYHRDLYNHLEEHEIGPSLYAAPWFLTMF ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD
5416	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTRS LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLRTSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEP RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKSFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIRSLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGKGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKRSGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQRLLAEQQ TLLAENYSELARAFGEPHSQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE

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			QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKNNLQFVGINGGYETTSSDDSSSD ESSSSESDDECDVIEYPLEEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5417	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF RRPRLASFGGMGTTSSLPSPVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQERKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCRASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTK AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQRLQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTERSVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQINININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELARAFGEPHSQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKNNLQFVGINGGYETTSSDDSSSD ESSSSESDDECDVIEYPLEEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVRAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5418	24	1133	SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQKAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGNDAEGSPFR GQRFDPAMFNISPGAVQF
5419	1395	259	GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAREG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR
5420	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR

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			ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/ LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV RAELIRAFGERE
5421	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLPHERIR ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/ LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV RAELIRAFGERE
5422	3	1263	SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF KAGCNWWHLSRDQAGVQRCDLGSSQPPPLGFKRFSCLSLPSSWD YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR TVFVSERELDWAKVMVEKSRMGVVPPGTQVEQLLYAKKLYDSAF HPDTGEKMNVIGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQWV NQSFNALVNYTNRNAASPTSVRQMALSYFTATTTAVATAVGMNM LTKKAPPLVGRWVPFAAVAAANCVNIPMMRQQELIKGICVKDRN ENEIGHSRRAAAIGITQVVISRITMSAPGMILLPVIMERLEKLH FMQKVKVL/SAPLQVMLSGCFLIFMVPVACGLFPQKCELPVSYL EPKLQDTIKAKYGELEPYVYFNKGL
5423	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG PASFPSSSSQSQLPPGAAIQGSGDPEGQNPCFLRSFVRAHDSAG EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE NTPVLEDVIGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP DKKPMAAMEHPCEGV
5424	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW

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			SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR SNLTSLK\SSLQLYRQFKDIDEHQSLTESVLQKGEILLQCLLE NTPVLEDVLGRIAKQSGELRSHADRLYDSILASLDMLAGCTLIP DKKPMAAMEHPCEGV
5425	1086	115	GFCPSPSLGHQPPRVLHPTMSMAVETFGPFMATVGLLMLGVTLP NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWRFPSML ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT KYELGPALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK NCSWEVAYLPSEAGSLIF
5426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGRALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLRKGTKHLSPYATLTVGDSSHKTETISQTSAPVWDESASPLI RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSRERFL LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5427	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVP DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL

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			ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSRREEL LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5428	3	1839	SSRSERLSACAIAPPWLVSSRPARPAQLQRPGKMVEDGAEELED LVHFSVSELPSRGYGVMEEIRRQGKLCDVTLKIGDHKFSAHRIV LAASIPYFHAMFTNDMMECKQDEIVMQGMDPSALEALINFAYNG NLAIDQQNVQSLLMGASFLQLQSIKDACCTFLRERLHPKNCLGV RQFAETMMCAVLYDAANSFIHQHFVEVSMSEEPLALPLEDVLEL VSRDELNVKSEEQVFEAALAWVRYDREQRGTPL\RNLQSNIRLL FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT I
5429	828	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF AQRERFHRFQPTYPYLQHEIDLPPTISLSDGEPPPYQGPCTLQ LRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNS GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFQHQQSSGPPSL LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL
5430	441	1507	QKRRKRRRKKIMKTIQPKMHNSISWAIFTGLAALCLFQGVPVRS GDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYA GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP TVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDV\A APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA EFQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSEHDYGNYT CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL HLLLKF
5431	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\ LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\ LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5433	360	1085	SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LPGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF SLIFTLGSFMNNPMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

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			IAPTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI ITTLYNGAPDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAPLTLAFP SEHPGKLFGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF MLAILLTFFHPFLVYRECRTWKESPSAIA
5434	66	652	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLQWLF/GSGK HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV LRQGRFGMPIGCINYPECEHTELIDKPDETAITCPQCRTGHLVQ RRSRYGKTPHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT AQGVKHFCASKQCGKPVSAE
5435	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPINVTLSSGFVADRGVKH HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEQSSSK GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAV TQKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA VHQKKEHSKNKCHKARRCHMNRTLEPNRRQKKNIWLETHIWHAK RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN KYPREMLGPVTPIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE IKAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKRKR KDDGENAKPIKKIIGDGTRDPCLPYSNISPTTGIIISDLTMEMN RFRLIGPLSHSILTEAIKAASVHTVGEDTERTPHRWWIETCKKP DSVSLHCRQEAIFELLGGITSPAEIPAGTTLGLTVGDPRINLPQ KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNQDICKSV TRNKISDQDLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKESAVH SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN YVKLGTLAPFCCPWEQLTQDNESRVQAYEEPSVASSPNGKESDL RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPR PHTMICVPAKEDPLQLHEDWHYCGPQESKHSDPFRSKILKQKEK KKREKRQKP\GRASSDGPAGEEPVAGQRALTLGLWSGPLPRVTL HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ RGLVLLRPPASLQYRFARIAIRV
5436	1781	635	ASDSIPWSEARTTRKLAQRGCQWSLPERMPLVVFCGLPYSGKSR RAEELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSARERKALRG ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA GSSVLRELHTADSVVNGSAQADVPKELEREESGAARSPALVTPD SEKSAKHGSGAFYSPELLEALTLRFEAPDSRNRWDRPLFTLVGL EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS QVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR QFISYTKMHPNNRNLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEPGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPE PRRVDSSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRAASE PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEKPGRREKLLGWLR GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA CLPGLLQALVLAVSLREPNGDEAATDWRSEGLEREGEEQRGDPG KGL
5438	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS LAPPSLRRPMMCQSEARQGPELRAAKNLKFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK NCEVEQVKGVTYSLESFLGPRMCTRDLPFPPAASCDSFKNQLVT

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			REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGRALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5440	693	253	EPIPVTPDHRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFNTLFMNTCCLG FIAPAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIFMT ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAPFSFIN NSDLWVANIETGEERRLTPCHQGLSNVLDDPKSAGVATFVIQEE FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVPSP ALEERKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE LVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLL PPALFIPSTENEEQ\RLASARAVPRNVQPYVVYEEVTNVWINVH DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW SEPFSPGEGEQSLTNAIWVNEETKLVYFQGTKDTPLEHHLYVVS YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY KLSGPDDDPLHKQPRFWASMMEAAKIFHFHTRSDVRLYGMIYKP HALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY AVVVIDGRGSCQRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKY GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVWM AYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER HSIRCPESGEHYEVTLLHFLQEYL
5442	1	3474	CGQRSRRRSPDMPEAKPAAKKAPKGKDAPKGAPKEAPPKRAPAE APKEAPPEDQSPTAEEPTGVFLKKPDSVSVETGKDAVVVAKVNG KELPDKPTIKWFKGKWLELGSKSGARFSFKESHNSASNVYTVEL HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRQDASGQSL ESFKRTSEKKSDTAGELDFSGLLKKRKVVEERKKKKKKDDDDLG IPPEIWELLKGAKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVK KSAAFTKKLDPAYQVDRGNKIKLMVEISDPDLTLKWFKNGQEIK PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV KEPPVLIVTPLEDQQVFVGDRVEMAVEVSEEGAQVMWMKDGVEL TREDSFKARYRFKKDGKRHILIFSDVVQEDRGRYQVITNGGQCE AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYK NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDYTFVPDGYAL GSLSAKLNFLEIKVEYVPKQ\EPPKIPLGFASGGKTSENAD/IV VVAGNKLRLDV\SITGEAPSPPAT\WLKG\DEVFTTTEGRTRIE KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIFLQVVDVP DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQ RWMKLNFEVFTETTYRSTKMIEGILYEMRVFAVNAIGVSQPSMN TKPFMPIAPTSEPLHLIVEDVTDTTTTLKWRPPNRIGAGGIDGY LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV NELGEALAECKLEVRVPQ

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5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSPRRSRSAAEPA MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKTDV NKIEEPLEEVLCPPKYLKLSPKHPESNTAGMDIFAKPSAYIKNS RPEANEALERGLLKTLQKLDEYLNSPLPDEIDENSMEDIKFSTR KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHQVKSRLLKEVS FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAY RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL IKVEAADMARAKALLGGPGEELEADTEYLDPFDAQPHPAPPDDG YMEPYDAQWVMSELPGRGVQLYDTPYEEQDPETADGPPSGQKPR QSRMPQEDERPADKYDQPWEWKKDHISRAPAVQFDSPEWERTPG SAKELRRPPPRSPQPAERVDPALPLEKQPWFHGPLNRADAESLL SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVV LGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTQTP*Q *PDWGDRRPNGQVATGLPELWGAEAPSAAAHPGLHRERHPEGLP RAEKPGLRGPLLGLREPLGAGPRGPWGLQEPRRCQVWFSQAPAH QGGGCGYGQSQGPSGRPRGGAGSRH
5445	2364	486	ILSRGFLGSVEICIQLPLPASEPVLLLTWARRRWRETRSRREPT TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP EEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEP ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTGHDSDKSD QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ DVLGIRQLERPLPLTSVCYPQDLPRPLRSREFPQFEPQRYPACA QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP ALPGQPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPG LPRHQDQPHHQPPNRAGAPGESLECPAELRPQVPQPPSPAAVPR PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLV NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKQ DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRPIPVLP PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGP LPTLQVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQ TLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLACTERPSKNSHP VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH MLFDRIRLVVTKGFSGTPGSNENSTQNVYKIPPTTTKALCPLYT TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA GGFLSKSLVFSVLFAVTLRSFVP*AHEPTRMSSDPQPHPSGSCA KGGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSEASTEHAGSFNATGQQKDTSGVAR PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHVPASHMPLAAA RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFQKKCEDCVVPY TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF IQPYLNSHYKETTVPRKVLPHLRGHRGPVNTIQWCPVLSKSHML LSTSMDKTFKVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL SGGFDFALHLTDLETGTQLPSGRSDFRITTLKFHPKDHNIFLCG GFSSEMKANDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD ASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALHPREPV FLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG GDLLVTGSADGRVLMYSFRTASRACTLQGHTQACVGTTYHPVLP SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL KSPSPSKSLLVLLCGRAMFQPATCPWQLPALSK
5448	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFPPPFF RWNLQVTSKVIPFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET

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			IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5449	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA HVKPDLIDVDLVRGSAFAKAXPESPWTSLTTKGIVRVVFPPFFF RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCST IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5450	8136	1242	GQQFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLLAAG PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTVV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGLP YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAGG RRGDPIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVSV HINAHRLRISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMA AGCRLEEEEYEDDAYGHYEAPSTLAPEAWPAMELPEPCVPEPGL PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELRK SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLGT SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTFR VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPAN LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWATQ AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSNL SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGPS PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYGA TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQGE SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLRAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE GVLVELEVLPAAIPLEAQNFSVPEGGSLTLAPLLRVSGPYFPT

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			LLGLSLQVLRPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT TNTGLQMWEGATAPIPAEALRSTDGDSGSEDLVYTIEQPSNGRV VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA GNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSPE AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSPQ RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGQLV YAHGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN ERPPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEVQ RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSQFQI DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR VVRVPRARTEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPGP AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV IIPMCLVLLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA GDTETPRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP ALKNGQYWV
5451	1	2274	RDSSEQGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR KNSEPGSPHSLEALRDAAPSQGLNFLLLPTKMLFIFNFLFSPLP TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV VVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKE SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ IDSLYEHIQD
5452	1833	1138	SRVPSLCLSLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG HIYNKNISQKDCDCLHVVEPMPVRGPDVRAYCLRCECKYERRSS VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ RKSVFDRHVVLS
5453	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVRSG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5454	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI

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			VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRRREQRQL*
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLQ WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT KALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFF DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT TAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA QKVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR DAQQQVKALGTRRTTLEGHLAKVQAQAEQGQQELKNLRACVLEL EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLQTSEA ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL QELKGNIRVFCRVRPVLPGEPTPPPGLLLPPSGPGGPSDPPTRL SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFEEIA MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPR ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDLLATGTRKG QGGECRIRRAGPGSEELTVTNARYVPVSCKKEVDALLHLARQNR AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVP MSMYRVRGGRVAGGCFIGWRAPCPRAIK
5457	2	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA LLRSARRLMRKVKKLRLDKENTGSWRSPSINSEGAERMATTGTP TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV RKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVPGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGCHQRLDQCS
5458	6642	4022	FVPGLREPQWEPAQPSATMSAPSKEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGSREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI QRGRLRDDIKEYKFREARLLQDYSELRRENISLQKQVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKRRQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTPSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLIAIIRDQIKHLQ AAVDRTTRLSRQRIASQELGPAVDKDKEALMEEILKLKSLLSTK

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			REQITTLRTVLKANKQTAEVALANLKSKYENEKAMVTETMMKLR NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDE KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGRP DLLATGVEREQSERFNVYILMPSPNLGCYMGECALQITYEYICLW DVQNPRVKLISWPLSALRRYGRDTTWPTFEAGRMCETGEGLFIP QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF PAYRSEH
5460	45	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK CEKCHHFFVVLSEADSKKSIIKEPESAAEAVKLAFQQKPPPPPK KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAE VEKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDIEEKDRL LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES SEEEYDSGVEEEGWPRQADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD SHRLPGDCFLLLVLLLYAPVGPCLLVLRLFLGIHVFLVSCALPD SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC ASTRLPPTPLLLFPEERATNGREGLLRFSSWPFSIQDVVQPLTL QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG EANEEFALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRP QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
5462	663	3353	KIKERQMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA RLSNGSPSAPSLTNSRGSVHTVSFLLQIGLTRESVTIRAQELSL SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILQLIT SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGMMVHYTSRDNLRK RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP KHFIMAPNPDDMEEDP
5463	237	1012	LLSVTMTTSRCSHLPEVLPDCTSSAAPVVKTVEDCGSLVNGQPQ YVMQVSAKDGQLLSTVVRTLATQSPFNDRPMCRICHEGSSQRDL

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			LSPCECTGTLGTIHRSCLEHWLSSSNTSYCKLCHFRFAVERKPR PLVEWLRNPGPQHEKRTLFGDMVCFLFITPLATISGWLCLRGAV DHL=IFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNEWR RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI LAFDVTDLESFEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA DRKYQSILENHLTESIKLSPDQSRSRCC
5465	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA VNVFHHLPYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK PHP?KRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC VWEMGTSKEKAKTVTLKQALLGHTDTVTCATASLAYHIIVSGSR DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG HSDGVVRFWRMEFLQVPETPAPEPAEVLEMQEDCPEAQIGQEAQ DEDSSDSRADEQSISQDPKDTPSQPSSTSHRPRAASCRATAAWC TDSGSDDSRRNSDQLSLDEKDGFIFVNYSEGQTRAHLQGPLSHP HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHFA EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDR GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI SSPVRVCQNCYYNLQHERGSEDGPRNC
5466	3	992	HACAHASAHASGRLVRWWRKRRSVMGIQTSPVLLASLGVGLVTL LGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKRF RFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQG YVDLVIKVYLKGVHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGL LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIR AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV QLACHPNLDKLGYSQKMRFTY
5467	2103	4	GRALRVGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSQEEWECLQPDQRTL YRDVMLENYSHLISLAGSSISKPDVITLLEQEKEPWMVVRKETS RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY FRNDSEYRQFEGLQGYQEGNINQKMISYEKLPTHTPHASLICNT HKPYECKECGKYFSCGSNLIQHQSIHTGEKPYKCKECGKAFQLH IQLTRHQKFHTGEKTFECKRCGKAFNLPTQLNRHKNIHTVKKLF ECKECGKSFNRSSNLTQHQSIHAGVKPYQCKECGKAFNRGSNLI QHQKIHSNEKPFVCKECGMAFRYHYQLIEHCQIHTGEKPFECKE CGKAFTLLTKLVRHQKIHTGEKPFECRECGKAFSLLNQLNRHKN IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG FNRGAHLIQHQKIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG DKPFECQDCGKAFNRGSSLVQHQSIHTGRKPYECKECGKAFRLY LQLSQHQKTHTGEKPFECKECGKFFRRGSNLNQHRSIHTGKKPF ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI RHQKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
5468	225	2976	SFLTDLFQSLAQLENLCKQLYETTDTTTRLQAEKALVEFTNSPD CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNNPLPLEQRIDI RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF RNAITDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIEA DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKQASGKNLNLND ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVQIPTSWR SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA SASPMDIAVQEGRLTWLVYIIGAVIGGRVSPASTDEQDAMDGEL VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQFRKIYIGDQVQ KSSKLYRRLSEVLGLNDETMVLSVFIGKIITNLKYWGRCRPITS KTLQLLNDLSIGYSSVRKLVKLSAVQFMLNNHTSEHFSFLGINN QSNLTDMRCRTTFYTALGRLLMVDLGEDEDQYEQFMLPLTAAFE AVAQMFSTNSFNEQEAKRTLVGLVRDLRGIAPAFNAKTSFMMLF EWIYPSYMPILQRAIELWYHDPACTTPVLKLMAELVHNRSQRLQ

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			FDVSSPNGILLFRETSKMITMYGNRILTLGEVPKDQVYALKLKG ISICFSMLKAALSGSYVNFGVFRLYGDDALDNALQTFIKLLLSI PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNQ ESDRFLHIMQQHPEMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG LILLNEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNLL TKNRDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DQEFETSLVPWHLPMGWLCSGLLFPVSCLVLLQVASSGNMKVLQ EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTC VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ CYNTTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLL CYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQ EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGK SAWCPVEISKTVLWPESISVVRCVELPEAPVECEEEEEVEEEKG SFCASPESSRDDFQEGSEGIVARLTESLFLDLLGEENGGFCQQD MGESCLLPPSGSTSAHMPWDEFPSAGPKEAPPWGKEQPLHLEPS PPASPTQSPDNLTCTETPLVIAGNPAYRSPSNSLSQSPCPRELG PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNV LQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPA PVPVPLPTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGG QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLEASLCPA SLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNPVSVGPTYM RVS
5470	17	1418	TACRIRTSLNRGIAAVKRDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE
5471	1868	658	RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP
5472	1469	753	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIPGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDRMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV
5473	3	2119	FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLEELEKQMTS FYDSLGKINEIITVLERDAQSSALFKQKHQELLACQENCKKTLT LIEKGSQSVQKFVTLSNVLKHPDQTRLQRQIADIHVAFQSMVKK TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLEEKGDPEE LLRRHTEPFSQLDQRVLNAFLKACDELTDILPEQEQQGLQEAVR KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTELDRET

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			KLMPQEGSEKIIKEHRVFPSDKGPHHLCEKRLQLIEELCVKLPV RDPVRDTPGTCHVTLKELRAAIDSTYRKLMEDPDKWKDYTSRFS EFSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVTKRG ETLSWLKSRLKVLTEVSSENEAQKQGDELAKLSSSFKALVTLLS EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQARKILDTE NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPDRG HEELRKLESTLDGLERSRERQERRIQVTLRKWEREFETNKETVVR YLPQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQAEN LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYVIDK S
5474	2	780	TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQSTI LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINIRTG QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAWKFT LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGRTLS LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYGQQ PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF
5475	2	506	ARGWLESLSLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGYYRF VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTL STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQK GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR
5476	192	1457	SDSMSLLDCPCTSRTQVESLRPEKQSETSIHQYLVDEPTLSWSR PSTRASEVLCSTNVSHYELQVEIGRGPDNLTSVHLARHTPTGTL VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVFTVG SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGLN YLHQNGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQRHR AVYDFPQFSTSVQPWLSPELLRQDLHGYNVKSDIYSVGITACEL ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSESRMKNSQ SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLLSHVFFKQMKEESQDSILSLLPPAYNKPSI SLPPVLPWTEPECDFPDEKDSYWEP
5477	3	1044	RGNSRLRYSHEDELQLPRLPELFEIGRQLLDEVEVATEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEFE LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVRKYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSRRASTSNSSRQERPPVKPPILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG
5478	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5479	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5480	444	1952	LSLTSRMEEAELVKGRLQAITDKRKYQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEKAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR

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			LMTPWEESNVMQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCQE DEEDVRYNIVHSLPPDINDTEPVTMIPMGYQQAEDSEEDKKFLT GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQPAKP TPLPRKRSEASPHEKHKS
5481	3	1422	NSPGSVCLCQCVCPSLLHCLPPLLLLLLLPLLLHESPQPPALRV VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV QGLNKAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTLPAT ILTSLFTDSLVKEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR KELQKELQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT CIMNAVEWNKKEPLVAEQALKHLKQYAPLLAVFSSQGQSELILL QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEEAILKWYKEAHV AKGKSVFLDQMKKFVEWLQNAEEESRSEGEEN
5482	1492	528	THVVMTGMCYAFHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPA LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGP GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP VMVPAQSQAGSLV
5483	1	788	FPFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA ENRIKQLETDSSEEISRYQEMIQKLQNVLESERENCGLVSEQRL KLQQENKQLRK3TESLRKIALEAQKKAKVKISTMEHEFSIKERG FEVQLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA RIRINNLKSELSRQKLHTQELLSQLEMANEKVAENEKLILEHQR KANRLQRRLSQAEERAASASQQLSVITVQRRKAASLMNLENI
5484	3	1997	IMADMEDLFGSDADSEAERKDSDSGSDSDSDQENAASGSNASGS ESDQDERGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDNR SRASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDERAQGSDEDK LQNSDDDEKMQNTDDERPQLSDDERQQLSEEEKANSDDERPVA SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD EEEQDHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD NSGTMDLPGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE PIPETRIEVRIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESNAR IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTQKIRILPMAGRD PECQRTEMIKKEEERLRASIRRRSQQRRMREKQHQRGLSASYLE PDRYDEEEEGKESISLAAIKNRYKGGIREERARIYSSDSDEGSE EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEELTDQ AGTN
5485	161	1074	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY RGILPPLMQKTTTLALMPGLYEDLSCLLHKHVSAPEFATSGVAA VLAGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEPQSFPKVFQKI WLERDRKLINLFRGAHLNYHRSLISWGIINATYEFLLKVI
5486	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR PAAGKEAQKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS GSLATSISQMVKTEGKGAKRKTSREEKNGSEKLVEKKVCKASSV IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRVSY FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG DSRAILCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGGNVR DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL

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			ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
5487	535	182	AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTLALLLLAGLTA LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK CKCKSSQKQHSPVPEKAIPLITPGSATTC
5488	1072	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDYIEN LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGANLLL NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVKAVD TTVSFKI
5489	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP GEDEDS
5490	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP GEDEDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEGRSE QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEETSC LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCNTPKP SFFDPEGKQKWRAWKALGDSSPSQAMQEYIAVVKKLDPGWNPQI PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENNIDH ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLQHRAD INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDGCLP EEVTGCKTVSLVLQRHTTGKA
5492	3	1896	ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNIPYEATEE QLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM RNLNGREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGDP IDPEDAPESITRAVASLPPEQMFELMKQMKLCVQNSHQEARNML LQNPQLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSQ SVSVSGPGPGPGPGLCPGPNVLLNQQNPPAPQPQFLARRPVKDI PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGMPG VGPVPLERGQVQMSDPRAPIPRGPVTPGGLPPRGLLGDAPNDPR GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHEMRG GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMETE VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ GTGMQGAGIQGGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI LILKEQIQKSTGAS
5493	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKELECAREGEEERRREREVLREEIQTLTSKLQELQEM KKEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSEEGLPRP RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR

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			GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRSASAT HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP SLPTKNPPV
5494	71	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLLGT RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP GDEEAQVENLITANATEPQKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLPP QGAISETRMGHPQFWKYEPGACTGSLASLEQYSEQLKDMVAFFL GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVEMGDPELLGIKKL SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT GFPTHPNHEPPEETDGPPGAVALVAFLQALEKEVAIIVDQRAWN LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPQT PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADFA VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH AEMIQKLVDVTTAQV
5496	3	2408	QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDYSG MKSGKGRPISPVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSDTFFR PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLILLSE NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQANTLK SPVSESVSPVVPDYLPTRNGDFLSSKRKQISRDINRIRSVTVNH MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL SRNLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLEKGNKKNS TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC NRPVGSDQKAVIHSKSSPEISLRFESGPGAVINSLLAEKNGFLQ CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIQVSNTKINL KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT GNDLKENVKSDSVLLTSGKYDLKKQRSVTQATQTSPGVPWPSQS ANFPEPSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL HHIKKMTVE
5497	1821	3308	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV CFIYKYSGFPSLECQCHFVSPHSSCYINFPSFPPPPFFVCFQLSN GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH YYTIGPGMFPPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGEEMEACEELA LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPA STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK TPVIPVKTPTVPDLPGVLPAPPDGPEERGEHSPESPSVGEGPQG VTSMPSSMWSGQASVNPPLPGPKPSIPEEHRQAIPESEAEDQER EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT TTNDRSAPRFS
5498	2434	1492	ILTHQEIFTGEKPCECGKASIQMSHLSQQKIYSGENPFACKVCG KVFSHKSNLTEHRHFHTREKPFECNECGKAFSQKQYVIKHQNTH TGEKLFECNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI QKSNLIRHQRTHTGEKPFVCKECGKTFSGKSNLTEHEKIHIGEK PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

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			QKIHTH
5499	324	926	GFGQIGRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH WKVRNPEVHRGDIVSLVSPKNPEQKIIKRVIALEGDIVRTIGHK NRYVKVPRGHIWVEGDHHGHSFDSNSPGPVSLGLLHAHATHILW PPERWQKLRSVLPPERLPVQREER
5500	1978	1286	KPDWRLQNLPPRLYLWRSSRFGFGHLKKRLQMDFKIEHTWDGFP VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW DYEVVEAFFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL PLSFRVSRGETKWEGKAYLPWSYFPPNVTKFNSFAIHGSKDKRS YEALYPVPQHELQQGQKPDFHCLEYFKSFNFNTLLGEEWKQPSS DLWLIEKCDI
5501	2927	2226	CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP AAIMLALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFVNVIA SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDIGGQPRFRSMWERY CRGVNAIVYMIDAADREKIEASRNELHNLLDKPQLQGIPVLVLG NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT LQWLIQHSKSRRS
5502	3	824	NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIQ REIALAKKHGTQNKRAALQALKRKKRFEKQLTQIDGTLSTIEPQ REALENSHTNTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT EQQDIAQEISRAFSQRVGFGDDFDEDELMAELEELEQEELNKKM TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEREDDD IKQLAAWAT
5503	216.	654	KGVRRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT SPAGTLGEKPVKS
5504	58	3563	QLSFSFQAPVTFDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL GPTVANPELFRKFGRGPEPWLGSVQGQRSLLEHHPGKKQMGYMG EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDNAGRNRKL LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL IEGYTGPFKVETLKYHAKSKAHMPCVNALAARDPIWAARFRSIR DPPGDVLASPEPLFTADCPIFYPPGPLCGFDSMAELLPSSRAEL EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE SCIQDPSAEGLSEEVPVVFEELPVVFEDVAVYFTREEWGMLDKR QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAPWIKDPN GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARASC CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQFPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHRVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILRD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASPGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219	NCSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAYIEEFLQ QYNHYKSNVEIFKLQPNKPSKELAELVMFMAQISHCYPEYLSNF PQEVKDLLSCNHTVLDPDLRMTFCKALILLRNKNLINPSSLLEL FFELFRCHDKLLRKTLYTHIVTDIKNINAKHKNNKVNVVLQNFM

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			YTMLRDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACFSK VTKILVAALTFFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG KKSSKNKKKLLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPQDFA EKLLKQLECCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLQR FLQPHQREVTKILLFAAQASHHLVPPEIIQSLLMTVANNPVTDK NSGEVMTVGINAIKRITARCPLAMTEELLQDLAQYKTHKDKNVM MSARTLIHLFRTLNPQMLQKKFRGKPTEASIRARVQEYGELDAK DYIPGAEVLEVEKEENAENDEDGWESISLSEEEDADGEWIDVQH SSDEEQQEISKKLNSMPMEERKAKAAAISTSRVLTQEDFQKIRM AQMRKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDIERLHKK PKSDKETRLATAMAGKTDRKEFVRKKTKTNPFSSSTNKEKKKQK NFMMMRYSQNVRSKNKRSFREKQLALRDALLKKKKRMK
5506	1	1531	FRGDLCGQRGGSAPGEGGSSAWPAPAHPLPERERERREALCPGRS CSGGGGEETPGTTPVWSPLEGGGDRELRPNPYVRFPYRWWAVVV LAAFPSLGAGGETPEAPPESWTQLWFFRPVVNAAGYASFMVPGY LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT EAAETTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY SFASLSNVLSSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKLV SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL LEQGALLEGTRFMGRHSRFAAHALLLSICSACGQLFIFYTIGQP GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL LRVYARGRLKQRGKKAVPVESPVQKV
5507	3704	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIEITSEDRFIQ YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI GKEWQGIYYAKKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKCRRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI FELEAATHNRPLIYLGLRMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KFVNSINKPLATLEENGRTDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPR
5508	1151	691	LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGRSCQELREKFW EFYKADWCVWPAAQFVNFLPVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD
5509	1238	619	RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM RDFVTWVDSSKIKRHVLEYNEERDDFDLEA
5510	96	1195	PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF KFGSLLPIHPVTSG

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5511	276	1980	KLSRVLNLPPENLITSISAVPISQKEEVADFQLSVDSLLEKDND HSRPDIQVQAKRLAEKLRCDTVVSEISTGQRTVNFKINRELLTK TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKFHVG HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL FGYEEKLQSNPLQHLFEVYVQVNKEAADDKSVAKAAQEFFQRLE LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK SQEVLKLLESKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT SLYATRDLAAAIDRMDKYNFDTMIYVTDKGQKKHFQQVFQMLKI MGYDWAERCQHVPFGVVQGMKTRRGDVTPLEDVLNEIQLRMLQN MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR VFQSRGDTGVPLQYTHARLHSLEETFGCGYLNDFNTACLQEPQS VSILQHLLRFDEVLYKSSQDFQPRHIVSYLLTLSHLAAVAHKTL QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM
5512	120	1015	DPSLLLTITVTGVTVLVLVLKSMNSRRREPITLQDPEAKYPLPL IEKEKISHNTRRFRFGLPSPDHVLGLPVGNYVQLLAKIDNELVV RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK IGETIFFRGPRGRLFYIGPGNLGIRPDQTSEPKKTLADHLGMIA GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE EIARTHPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWRLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPPPEPSSFPS PPTSRGGPGSRDTMSDSEEESQDRQLKIVVLGDGASGKTSLTTC FAQETFGKQYKQTIGLDFFLRRITLPGNLNVTLQIWDIGGQTIG GKMLDKYIYGAQGVLLVYDITNYQSFENLEDWYTVVKKVSEESE TQPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG DSVFLCFQKVAAEILGIKLNKAEIEQSQRVVKADIVNYNQEPMS RTVNPPRSSMCAVQ
5514	1295	449	VNRPSWIMGNFRGHALPGTFFFFIIGLWWCTKSILKYICKKQKRT CYLGSKTLFYRLEILEGITIVGMALTGMAGEQFIPGGPHLMLYD YKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSLTKL MLSNALFVEAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFL EFLVRNNVLLELLRSSLILLQGSWFFQIGFVLYPPSGGPAWDLM DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS EVGLLKNAERQESEEEM
5515	1572	260	FVRLVGRGDCDPLLSVCLTTMPLYEGLGSGGEKTAVVIDLGEAF TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEELYSYL KEFIHILYFRHLLVNPRDRRVVIIESVLCPSHFRETLTRVLFKY FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP VLNCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVELLFEQDNEEQSVATLILDSL IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK
5516	3	735	NSREPPQAGPGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES IKAMWRVPGTTRRPVTGRSPGMHRPEAMLLLLTLALLGGPTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR
5517	246	499	SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK
5518	3	1375	DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EPKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSMNPDGFEAVKKPDCYYSIGRWNYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETPVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLQGGMQDYNYIWAQCFEITLELSCCKYPREEKLP SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK

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			HICPYRTNKYGEYYLLLLPGSYIINVTVPGHDPHITKVIIPEKS QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT KPSLFLFLVSLLHIFFK
5519	87	477	IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAAVAAVVG GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS
5520	117	943	PTEGRQKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYTFLNYYI SQEGKDEVKPKILANGARWKYMTLLNLLLQTIPYGVTCLDDVLK RTKGGKDIKFLTAFRDLLFTTLAPPVSTFVFLAFWILFLYNRDL IYPKVLDTVIPVWLNHAMHTPIPPITLAEVVLRPHSYPSKKTGL TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLAAFPSLS YVFIASIYLLGEKLNHWKNVSVQILQRWRLESVGICFQWPDWKS PAKHQLVKNIR
5521	546	911	KILNMQKSCERNEGKPQNMPKAEEDRPLEDVPQEAEGNPQPSEE GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDELER LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
5522	1224	637	GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYITNYSRRF WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEKADEHL FALEKLVKERLEGKQNLNCI
5523	3	1280	SKGKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELEILQEIE HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPG FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRD SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES RDAAEPVEDEAERSALPMCGPICPSAGSG
5524	85	2318	RERERDHRPGESSQGQSGAGGCFPSPTMELRCGGLLFSSRFDSG NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEFNVWTRPD CAETEPENGNRSWFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGA TTFFAFCYPPSYSDCQELLNQLDQRFPENHPTHSSPLDTIYYHR ELLCYSLDGLRVDLLTITSCHGLREDRRPRLEQLFPDTSTPRPP RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLR RLFVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLKPDAVLHPA IYGAKAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKAN NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWIMPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSPSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK
5525	105	834	SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP
5526	3	853	RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEEHLEKHRKDK AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL YYRRAHRRFVTKKALCIRVPQETQKLKKRRRALRAAAAAQKQAK

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			RRNPDSPAKAIPKTLKDSQ
5527	3225	565	LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRPKQSSCG KFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELTDYQLVS PAKNPSSLFSKEAPKRKAQAVSEEEEEEEGKSSSPKKKIKLKKS KNVATEGTSTQKEPEVKDPELEAQGDDMVCDDPEAGEMTSENLV QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHDQKADVS AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDKLDILGA AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGETRTE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEARAKTGGT VSDQALLPGDDDAGEGPSSLIRRKPVPKQNENEEENLDKEQTGN LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPK RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFLMQYPG RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQRLRNLEQ FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLFTESQKTK YPTQSGKPPLLVSAPSKSESALSCLSKQKKKKTKKPKEPQPEQP QPSTSAN
5528	3	895	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFE YVRDFEADDTCLAHCWVVVRLDGRNFHRPAEKHNFAKPNDSRAL QLMCKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQT LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTL AADKNEILFSEFNINYNNEPPMYRRGTVLIWQKVDEVMTKEIKL PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL
5529	48	640	TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL LSWTLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDPE KPNTLEELEVVSESCVEVQEINEERYLVIIRFTPTVPHCSLATL IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV AAAMENPNLREIVEQCVLEPD
5530	4541	2606	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEHN SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEEDEEDKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFFSDHMADTTTRLERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI
5531	24	515	GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLRHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE
5532	3395	1402	SDWMVVGKRKMIIEDETEFCGEELLHSVLQCKSVPDVLDGREMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS RPANSERYVVCKGLKVGIDDVRDYLPAVNIKLNQLRNTDSDVNL

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			VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTL SEPRQAEIRKECLRLWGIPDQARVAPSSSDPKSKFFELIQGTEI DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSQI YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAQRKI SAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF VPMGLYIVRTVNEPWTMGPSKSPKKKFFYNKKTKDSTFDLPADS IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ MHRA
5533	94	789	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP TVFENYTACLETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSELISPT FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK CAFLLFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTQDETQKSDSENEDLKIDCLQESQEL NLQKLKNSERILTEAKQKMREITVNIKMKEDLIKELIKTGNDAK SVSKQYTLKVTKLEHDAEQAKVELTETQKQIQELENKDLSDVAM KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN ELEQSVDHMKYQKIQLQRKLQEENEKRKQLDAVIKRDQQKIKVI LSYIPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPPSAAPLPTGRAQMSP SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP DAVYTELQPTSPTPTWPADETPQPQTQTQQLEGTDGPLVTDPET HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGFHEDDPF FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537	3	2391	RARVSSPQLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLEN YRNLVSLGLVVSKPDLITFLEQRKRPWNVKSRETVAIQPDVFSH YNKDLLTEHCTEASFQKVISRRHGSCDLENLHLRKRWKREECEG HNGCYDEKTFKYDQPDESSVESLFHQQILSSCAKSYNFDQYRKV FTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG EKNYHCNNSEKTLNQSSSPKNHQENYFLEKQYKCKEFEEVFLQS MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTQHQIIP TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR EKL
5538	926	161	HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA
5539	38	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK DEIYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCS SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL

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			ELEKVHDLCDNFCHRYITCLKGKMPIDLVIEDRDGGCREDFEDY PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS LNLEGEWHYL
5540	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5542	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGRD EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG SSASRDRVLARTMIVADSECRAELKDYLRFAPGGVGDSGPGEEQ RESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKLRKLSEINK LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLS SFVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF ESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESLL VTPSADILEPSPHPDMLCPVEDPTPGYEDPTRRGAQAPPTFRAQ DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTV ACYPEKTTRRMYNLFWRHFRHSEKVHVNLLLLEARMQAALLYAL RAITRYMT
5544	1895	514	LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD PEGRRQEPLRRRASSASVPAVGASAEGTRRDRLGSYSGPTSVSR QRVESLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAEEEEEEV ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRRGNLHFIR FPTHDMPAFIQMGRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD LQLCKLDELDCLIKGILYIDSVGFNGRSQCYYFENPADSEKCQK LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKRVTGTSLGGGTF FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRDIYGGDYERFG LPGWAVASSFGNMMSKERREAVSKEDLARATLITITNNIGSIAR MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSKGQLKALF SEHEGYFGAVGALLELLKIP

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5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVL KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSNNQEV SAFGEDGEGDDLDLWTVRCSGQHWERBAAVRFQHVGTSVFLSVI GEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIPIKPSVEPSAGH DRL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH RKKSLEGMKKARVGGSDEEASGIPSRTASLRLGEDDDEQEDDDI EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA
5548	1	2153	DQTGPPETTAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLLVLLLAAYFFRP RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVKDFW RMIWEWKSHTIVMLTEVEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK
5549	915	256	FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
5550	2364	1210	RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTNMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETNVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH
5551	211	1700	MQRDHTMDYKESCPSVSIPSSDEHRKKKKRFTVYKVLVSVGRSE

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			WFVFRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE DERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKV LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKH PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQRERSFPEHRAR FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDFGLC KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY EMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELL EKDRQNRLGAKEDFLEIQNHPFFESLSWADLVQKKIPPPFNPNV AGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAPVG FSYAPPSEDLFL
5552	2748	930	LGPAAGAAMGKKHKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG SSVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKSEKEKHL DDEERRKRKEEKKRKRREREHCDTEGEADDFDPGKKVEVEPPPDR PVRACRTQPARNESTPIQQLLEHFLRQLQRKDPHGFFAPPVTDA IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA MTYNRPDTVYYKLAKKILMAGFKMMSKQAALLGNEDTAVEEPVP EVVPVQVETAKKSKKPSREVISCMFEPEGNACSLTDSTAREHVL ALVEHAADEARDRINRFLPGGKMGYLKRNGDGSLLYSVVNTAKP DADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLSSATT ALSMQNNSVFGDLKSDEMELLYSAYGDETGVQCALSLQEFVKDA GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS HLNLDETTKLLQDLHEAQAERGCSRPSSNLSSLSNASERDQHHL GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAKQEPFHVVTPLLESWALSQVAGMP VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGI AAAYAARKLGIPATIVLPESTSLQVVQRLQGEGAEVQLTGKVWD EANLRAQELAKRDGWENVPPFDHPLIWKGHASLVQELKAVLRTP PGALVLAVGGGGLLAGVVAGLLEVGNQHVPIIAMETHGAHCFNA AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLQAEGCL PPSLTSVVVIVCGGNNINSRELQALKTHLGQV
5554	166	2310	CSGRTGGRGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL GRSFPWVLFPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVRKDVGLSDEEKLFQ VHTPEIFQKKLNESENSVFQAVYGLQRALQGDYKDVVNMKESSR QRLEALREAAIKEETEYMELLAAEKHQVEALKNMQHQNQSLSML DEILEDVRKAADRLEEEIEEHAFDDNKSVKGVNFEAVLRVEEEE ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPERLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMRSKGNKRILILGISAPIFLMLTVTELLDVSMELGCFLAGAL VSSQGPVVTREIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SSFSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL
5555	212	1425	LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY
5556	5835	3346	RTRGMSKNCVPMEFEEYLLRMFQGTFYLLQKITKDNNAHTVKSR

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			LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLFK YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVHSINHASLI SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVENI SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL TLFRGLRVQMGVPPTEQIIQTFLNMFTREQLAESILHEGSTGCR VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENEP QFSAIMQAFGQSFLQPDIHLFKQNLPYLETLNTKQKLYHKKIFR TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA APLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAATR KHLPARNHCGLSDSSPQLWPEPDFRNPPRKASKASLDFKRYVTD RRLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLRAGAKVV ALESDKTFIPHLRSLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP AMSSRGLFKNLGIEAVPNTADIPLKVVGMFPSRGEKRALWKLAY DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVLSVI WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRRLLDQLQQKLY LIQMIPRQNLPTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY KWLYDETLEDR
5558	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA GLFQCQKEGPIIIHTDEADSEVLYPNYQSCMSLRQRTRGRRQTA SLQPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPS CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKNPP FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF LNAMSVYTLSPEKYHALCSQTQVMEVGNKE
5559	150	1983	PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELEK ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDSDLG KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA VDKKEAGKDGRGEERAVATKKEEKKGSDRNTGLSRDKDKKREE MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG PTKPSEGPAKVEEEAAPSIFDEPLERVKNNDPEMTSVNVNNSDC ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAN KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHICG GKTEMEIAKLLKENTTLLKLGYHFELAGPRMIVTNLLSRNMDKQ RQKRLQEQRQAQEAKGRKKDLLEVPKAGAVAKGSPXPSPQPSPK PSPKNSPKKGGAPAAPPPPPPPLAPPLIMENLKNSLSPATQRKM GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
5560	9	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAM QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK IRFFFERGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS FKVQTLARSIGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL SDRSRQAYTFHLMEASGTTWSPENWLQPTAELPFPQLYT
5561	2175	1775	CYFIFQFFSSPYPGLHPHQTPAPLPNPGLYPPPVSMSPGQPPPQ

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			QLLAPTYFSAPGVMNFGNPSYPYAPGALPPPPPPHLYPNTQAPS QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVTIKPPPPEVVSRGS S
5562	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC VPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCT GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV TATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQETSLP
5565	993	138	RWNSPNPARAGSISRPQRAPGSVSAVAMTAAVFFGCAFIAFGPA LALYVFTIATEPLRIIPLIAGAPFWLVSLLISSLVNFMARVIID NKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSIN PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH GDSPQPFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS LKLCLLCQDKNFILYNQRSR
5566	2043	1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT KNVKEYVRWMMYWIVFALYTVIETVADQTVAWFPLYYELKIAFV IWLLSPYTKGASLIYRKFLHPLLSSKERBIDDYIVQAKERGYET MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTTIQG DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEEA EGPYSDNEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVKK RPQVYF
5567	1554	233	EFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEAGANINA CDSECWTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLQ AGADLHAPLDHGATLLHVAAANGFSEAAALLLKHRASLSAKDQD GNEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDETPLDVCGDE EVRAKLLELKHKHDALLRAQSRQRSLLRRRTSSAGSRGKVVRRV SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDDRQTGAELR PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPESPETAEP GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM
5568	1731	587	AEDRQPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL SLLVSGPRLFLLQQPLAPSGLTLKSKALRNWQVYRLVTYIFVYE NPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG MVVPSVLVPWLLLGASWLIPQTSFLSNVCGLSIGLAYGLTYCYS IDLSERVALKLDQTPPFSLMRRISVFKYVSGSSAERRAAQSRKL NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP VNSPGTVYSGALGTPGAAGSKESSRVPMP
5569	2	835	QTPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG

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			LKLLLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP KGEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPG PMGIPGEPGERGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL TNPQGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLLYRSGVK VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG SDSVFSGFLLFPD
5570	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEPVVKFYGPQGT PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH RPEEYKQKIKRYIQKYATEEALKEQEEGTGDSSSESSMSDFSED EAQDMEL
5571	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEPVVKFYGPQGT PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH RPEEYKQKIKEYIQKYATEEALKEQEEGTGDSSSESSMSDFSED EAQDMEL
5572	2802	2085	RTDYRTGIPGRRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG DAGAAAEGGGWAAAALALLTGGGEMLLNVALVALVLLGAYRLWV RWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDGSRNP RILLAVNGKVFDVTKGSKFYGPAGPYGIPAGRDASRGLATFCLD KDALRDEYDDLSDLNAVQMESVREWEMQFKEKYDYVGRLLKPGE EPSEYTDEEDTKDHNKQD
5573	2562	219	VPARTPNAEDQGPEARAATATPCQSGGRERAGEAAEDGVKMAAF SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWQ MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN QALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK SQHSGNAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLFRTF
5574	1731	952	NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
5575	456	766	LLNALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP
5576	249	2146	RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV DQKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLEQYVKQLQVVRVVRQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIAEDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFCWETLPPHEKQRR KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMEIWGGENVEM

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			SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFPKGTSVIARNQVR LAEVWMDSYKKIFYRRNLQAAKMAQEKSFGDISERLQLREQLHC HNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNQCLDVGENNRG GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLHVSKGALG LGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKKPA MAPCNPSDPHQLWLFV
5577	3	1275	RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKLILLPVLLD YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTL SPGEHAKDEYVLYYYSNLSVPIGRPQNRVHLMGDILCNDGSLLL QDVQEADQGTYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRM SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS IHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIV GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIK EKPCHPERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPV WPSLRSDRNNSLEKKSGGGMPKTQQAF
5578	3	783	AVESMASPGAGRAPPELPERNCGYREVEYWDQRYQGAADSAPYD WFGDFSSPRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLDFPSASFDVVL EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYLMHKGGK LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL
5579	3	1540	RNSGLARGASALARHGGGLAGGVGWDCGACASRCQGVMEGLLTR CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQPQNL REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPYTV RAMEKLVRVIDQEMQAIGGQKVNMPSLSPARLWQATNRWDLMGK ELLRLRDRHGKEYCLGPTHEEAITALIASQKKLSYKQLPFLLYQ VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALKDPAHF EVWCQNTGEVAFLTKDGVMDLLTPVQTV
5580	1681	450	ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAAPGLTAP WRLLQCCKLRAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELPRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLPGLPNDS
5581	54	947	GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW
5582	5775	2739	IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETPSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDPSDGDVPGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVPPGGTPLLPPVVGGSIPVSSPLPP ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL

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			DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPSPEPCMPN TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK RDILLGRLRSSEDQTWKRIRPRPTKTSPVGSYYLCKDMINKQDC KYGDNCTFAYHQEEIDVWTEERKGTLNRDLLFDPLGGVKRGSLT IAKLLKEHQGIFTPLCEICFDSKPRIISKGTKDSPSVCSNLAAK HSPYNNKCLVHIVRSTSLKYSKIRQFQEHFQFDVCRHEVRYGCL REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAH AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNSQVVEPDKDLK YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL CGKNSNSKKQWQQHIQSEKHKEKVPTSDSDASGWAFRFPMGEFR LCDRLQKGKAGPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAR KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE
5583	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA
5584	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA
5585	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5586	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5587	1768	148	SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA

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			CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKQSRI RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF DFGEKQKNALGEAARAAGFNVLRLIHEPSAALLAYGIGQDSPTG KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS ANCPLDSLYEGQDFDCNVSRARFELLCSPLFNKCIEAIRGLLDQ NGFTADDINKVVLCGGSSRIPKIQQLIKDLFPAVELLNSIPPDE VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET GKCEAISIEIAS
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN VLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV RPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS PRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF RPPAQWSSLIGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALM KEIEAAGEALQSVHAVPSAPAVPSGTGQTSAELEVQRRHSLVSF VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGF TFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARV TLLRLRQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLW SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPGSGLDLADA LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKPDKG KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY QQKKFCFSIQQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAE PPPPPEPARI
5591	68	1494	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLV PVPVSEPVPEPEPEPEPEPKPVKEEKLSPEPILVDTASPSPMETSG CAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYL RQLEEEQAVRPKYLLGREVTGNMRAILIDWLVQVQMKFRLLQET MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPEI GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALK ILDNGEWTPTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG VGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILD TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK MLTKISS
5593	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAR DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR SLDLYDNQIKKIENLEALTELRILDISFNLLRNIEGVDKLTRLK KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV

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			MLALPSVRQIDATFVRF
5594	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLRELQSLR ELDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV MLALPSVRQIDATFVRF
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE PIALAWSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD VFSVIGVRPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA HTTLAYGLNQEEFTDGREEEEEEDTAAGEPSRDTRGAAGPLDKG GSWCDS
5596	698	219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP VFVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIQRPR PCGGPHTAVGTKYGMPSSHSQFMWFPSVYSFLFLYLRMHQTNNA RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW FEYTVTRAEARNRQRKLGTKLQ
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPERRVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLRFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYPSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPERRVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDPTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

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			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC TFYHPTINVPPRHALKWIRPQTSE
5601	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC TFYHPTINVPPRHALKWIRPQTSE
5602	246	766	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC AAALRLMKIPLVVYGCQNERFGGCGSVLNIASADLPNTGRPFQC IPGYRAEEAVEMLKTFYKQENPNAPKSKVRKKECQQILNMF
5603	1	565	FRGRTPISGGRRGCAQYPIPATPARSGENRTMPGAGDGGKAPAR WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS CFGFEDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLQHHA TIFLQVVDRRMQ
5604	1	1506	EDIFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN
5605	35	1821	SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGRETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLVQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT
5606	3	1099	GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IEECQYQFRNRRWNCSTLDSLPVFGKVVIQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR TCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKC RQCQRLVELHTCR

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5607	521	141	PPVCNPAEAMPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRV QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
5608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV RIQTEPKYTGIWHCVRDTYHREGVWGFYRGLLLPVCTVSLVSSE VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPEP KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFLSYA VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL QADGQGQRRYRGLLHCMVTIVRREGPRVLFKGLVLNCCRAFPVN MVVFVAYEAVLRLARGLLT
5609	1628	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD ALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY RNQKFKCGEDNDGVSVKMKMKYYIEYMESTRDDSPLYIFDSSYG EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWPVMGPPRS GTGIHIDPLGTSAWNALVQGHKRWCLPPTSTPRELIKVTRDEGG NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFVPGG WWHVVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYR ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSDSD SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKRRSSS R
5610	54	1196	LERTPASADMAWTKYQLFLAGLMLVTGSINTLSAKWADNFMAEG CGGSKEHSFQHPFLQAVGMFLGEFSCLAAFYLLRCRAAGQSDSS VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR LSRGRPLAEESEQERLLGGTRTPINDAS
5611	2	577	FVLPNRLGIPGSTFRGPGACAESSSLAASAKPGAGGSPALAMSG ELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDRENLPE KLTAFKEKYMEFDLNNEGEIDLMSLKRMMEKLGVPKTHLEMKKM ISEVTGGVSDTISYRDFVNMMLGKRSAVELKLVMMFEGKANESSP KPVGPPPERDIASLP
5612	1	721	ASRDGYMDATIAPHRIPPEMPQYGEENHIPELMQAMWLCKHLNS SLLTLENLILNEFSYTATRARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISKLET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLIGPVGS
5613	115	1279	RGVDPALRRAEKMLPLSIKODEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5614	3	1268	LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQGQGETQNER APWGARQRLGVMAELQQLQEPEIPTGREALRGNHSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPAAVEVP QRPPTLEELSPPPPDEELPLPLDLPPPPPLDGDELGLPPPPPGF GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY

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			SDGWCEGVSSEGTGFPPGNYVEPSC
5615	9	1558	ALGRRRPGDPREMEAAATPAAAGAARREELDMDVMRPLINEQNF DGTSDEEHEQELLPVQKHYQLDDQEGISFVQTLMHLLKGNIGTG LLGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR FKKSTLGYSDTVSPAMEVSPWSCLQKQAAWGRSVVDFFLVITQL GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVD LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIYQ YVVRNMPDPHNLPIVAGWKKYPLPFGIAVFAFEGIGVVLPLENQ MKESKRFPQALNIGMGIVTTLYVTLATLGYMCFHDEIKGSITLN LPQDVWLYQSVKILYSFGIPVTYSIQFYVPAEIIIPGITSKFHT KWKQICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGFLLGTYITV EEIIYPTPKVVAGTPQSPFLNLNSTCLTSGLK
5616	1	719	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLAL HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDD KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV YAFLQTKVPQRSQKASVTP
5617	176	765	PWRGRGSRPRGAGAMAEEQVNRSAGLAPDCEASATAETTVSSVG TCEAAGKSPEPKDYDSTCVFCRIAGRQDPGTELLHCENEDLICF KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENMVTVGKTIL ERNNFTDFTNVRMGFHMPPFCSISHLHLHVLAPVDQLGPLSKLV YRVNSYWFITADHLIEKLRT
5618	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES LFLNSGGDSLKSIRLLSEIEKLVGTSVPGLLEIILSSSILEIYN HILQTVVPDEDVTFRKSCATKRKLSNINQERASGTSLHQKAIMT FTCHNEINAFVVLSRGSQILSLNSTRFLTKLGHCSSACPSDSVS QTNIQNLKGLNSPVLIGKSKDPSCVAKVSEEGKPAIGTQKMELH VRWRSDTGKCVDASPLVVIPTFDKSSTTVYIGSHSHRMKAVDFY SGKVKWEQILGDRIESSACVSKCGNFIVVGCYNGLVYVLKSNSG EKYWMFTTEDAVKSSATMDPTTGLIYIGSHDQHAYALDIYRKKC VWKSKCGGTVFSSPCLNLIPHHLYFATLGGLLLAVNPATGNVIW KHSCGKPLPSSPQCCSQYICIGCVDGNLLCFTHPGEQVWQFSTS GPIFSSPCTSPSEQKIFFGSHDCFIYCCNMKGHLQWKFETTSRV YATPPAPHNYNGSNEMLLAAASTDGKVWILESQSGQLQSVYELP GEVFSSPVVLESMLIIGCRDNYVYCLDLLGGNQK
5619	2160	1477	DSPVLPTSGNVISTAQPAQPWSAVRAALRSLGSPPGAGRGCPCP AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGHCSVL LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQPPLGP TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA ECSPPATP
5620	930	182	PLPPPTLAMPLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGCAMSG LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLALQFG EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEEKLNA TNIELATVQPGQNFHMFTKEELEEVIKDI
5621	3	819	VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA ENDLTWVLKHCERPLKQQQTSIKSSLLCLQGNYAGHDWFVSSLF MIMLGDKEKTFQFLHQFSRLLTSAFLWLPRLHISSYLPNDTVES GIHPVYFCSTHYIEMLLKAELPLVFSAFHMSGFAPSQICLQWIT QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDILQ HTQTQDLQVFLKREALHGFRVSDYFEYMEILEQNYRTVLLRDMR NIRLQST
5622	1122	456	AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAMY PGTFYFQFKNLWRANDRNETMLCFTVEGIKRRSVVSWKTGVFRN QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA GEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV

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			EIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL Q
5623	3	954	FLPFFIRAPKISRNGQWLFTPTTPFPFANKALPGWEGIVPACFW RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLRAANNSLVV TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT SQSQVIGFEGGKNASTSATSRSYSSIILPVVIALIVITLSVFVL VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH SAQGKTKN
5624	159	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKELYSLN EKKLLELRTEIVALHNQQDRALTQTDRKIETEVAGLKTMLESHK LDNIKYLAGSIFTCLTVALGFYRLWI
5625	1	1180	TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP AGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPP TAPDRATAVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCR VYPVQRALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE ILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKI RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILPIIFGTMEEMQNKAVVPFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGQKKKKIH
5627	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN LTVRFCILGKRSFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILPIIFGTMEEMQNKAVVPFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGQKKKKIH
5628	75	1455	VAGAMASKCLKAGPSSGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE QLQSCQAEIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVANAMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN PAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKMGKYFSLIPTGP

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			ADEDINKRFLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFAGVSDV DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV NQFALASHPFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP EVTALKVPE
5630	1194	278	GFWAIAQTCAHHLPPGSPWLVPASPWRLPEMSSFGYRTLTVALF TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM KSNVSVYQPPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLT LFLFRGNETLHYETPGKAAPAPQEATATFNSTADREDGHRNFSC LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP
5631	1053	290	SRVDDFVRPEPSRAEPSRSGRRRPARRAATMSVFGKLFGAGGGK AGKGGPTPQEAIQRLRDTEEMLSKKQEPLEKKIEQELTAAKKHG TKNKRAALQALKRKKRYEKQLAQIDGTLSTIEFQREALENANTN TEVLKNMGYAAKAMKAAHDNMDIDKVDELMQDIADQQELAEEIS TAISKPVGFGEEFDEDELMARLEELEQEELDKNLLEISGPETVP LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
5632	3	952	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD FTPVSSADAKDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMPMPSLGP NRQVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWIITIWIFGS LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE VVSTLIKLFGVFWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY FLSLYTGV
5633	771	460	QGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL LLLLLSGHRPWGSSMV
5634	1446	855	PRATGRIRSRAAASRPRAGAGASGAEPRSGRERSRLSGRRAPAM ARNTLSSRFRRVDIDEFDENKFVDEQEEAAAAAAEPGPDPSEVD GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK ALAVGGLGSIIRVLTARKTV
5635	3	943	DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL GVRRAVLQLPGLTQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAKANRALA HYRWW
5636	2253	1143	LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVPMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSPSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESVETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR
5637	948	2532	MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHLPHLPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAAMLNPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA

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			THEAVHLLCRMLVFDPYKRISAKDALAHPYLDEGRLRYHTCMCK CCFSTSTGRVYTSDFEPVTNPKFDDTPEKNLSSVRQVKEIIHQF ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSEMPPSPLVWE
5638	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5639	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5640	280	1092	QQGNKKTMLSHNTMMKQRKQQQATAIMKZVHGNDVDGMDLGKKVS IPRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNPDNIAP GYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLEALYPK LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLL LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT VPESEDL
5641	27	332	CRHNCNGDVKLLSNQMDKLFAFHLFTFHGLLHFLDGSIQKLIQA EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS NGESFVLSMIVTG
5642	199	1247	ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQ IFSCIIPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY TWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGIIT KANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWC VHRFDHHCVWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIQYLFLTFPRIVFM LGFVVVLSFLIGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCPL VAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAPPCHERKKQE
5643	1	847	PSGGVRDVETRGPGSRAARGPRVVMERRGVGAGAIAKKKLAEAK YKERGTVLAEDQLAQMSKQLDMFKTNLEEFASKHKQEIRKNPEF RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYYELGVQIIEVC LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLQLAEKNGYVTVS EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPALF TDLYSQEITAEEAREALP
5644	83	1138	PRRMGSWVQLITSVGVQQNHPGWTVAGQFQEKKRFTEEVIEYFQ KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALRD ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHQSLKAG
5645	537	799	VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD
5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFPEELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELPPRLQTHL RAEGGAQ
5647	288	800	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY

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			QRVLPLPIFTPAKMGATKEEREDTPIQLQELLALETALGGQCVD RQEVAEITKQLPPVVPVSKPGALRRSLSRSMSQEAQRG
5648	7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLQQAGNTDWSLTM APQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEPALTNPEK SSTKETERKETKAEEELDAEVLEVFHPTHEWQALQPGQAVPAGS HVRLNLQTGKREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQD LLSPGGLQVVINGLNSTEPLVKEYAAFVLGAAPSSNPKVQVEAI EGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLK LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFAEKEAELT QEMSPEKLQQYRQVHLLPGLWEQGNCEITVHLLALPEHDAREKV LQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE DEGYFQELLGSVNSLLKELR
5649	1172	3006	MLQEQLDAINEEIRMIQEEKRSTELRAEEIETRVTSGSMEALNL KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAR*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS
5652	735	343	HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA
5653	66	1401	RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDPTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ GWLLELQFRRSLYRGHLVR*FARRSRKSSEV*YCHQRGKSHGMQ

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			ES*IKERTQSCVHRPHGRRFHG\DNVSEKTLTPAKSKEYRGEPF SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK PTVHQECEQGFDRKASHSGYPKTHTGYKPYVCNEYGTPFSQSTY LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIQHQK THAANV
5654	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINQRRDSVRMSAL NWKPFVYGGLASITAECGTFPIDLTKTRFQIQGQTNDAKFKRII YRGMLHALVRIGREEGLKALYSG*VGLHAPLCHCSLFHMGIDFR PRLHRSQVKSLRCV*KEQIA**/MFSLLISTLISKYIYYAADVL EKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGDPELC ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNES EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	PRRVPPLPEFASGPGAAPFHSGRLQRSLTKDSAGCFSQCRSRAM LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLK PSNMNAFMENLEKNIHLRTSYSELVGFWSVEFGGRTNKVFHIWK YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP NSKLQKPPKEGVYELAVFQMKPGGPALWGDAPERAINAHVNLGY TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDPISWG GVRESVNYL\VSQQNM
5657	105	1052	GQRLQSPRVQMPVQPPSKDTEEMEAEGDSAAEMNGEEEESEEER SGSQTESEEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEXL FRERLSQLRLRLEEVGARRAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL
5658	2346	3541	TERRVYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLEDIWVTLSELDNVTPSFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHPSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSQAAEDLQQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST TAVRIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL
5659	2	696	WKRSGEVSPKGELGAWRGNSGRPKIIGRAARAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKARAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL
5660	229	853	PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE QRKAFPHHREFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL AGMAVTCDPKAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP SLAVHMHERGMDMDGEQKWQYRGRT
5662	2	1318	LRKEGRCRRGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSSA PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

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			LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR QNVELKAEKIKVIGNCDAKDFPIKYKERHPLEYLRQYPHFRCRT NVLGSILRIRSEATAAIHSFFKDSGFVHIHTPIITSNDSEGAGE LFQLEPSGKLKVPEENPFNVPAFLTVSGQLHLEVMSGAFTQVFT FGPTFRAENSQSRRHLAEFYMIEAEISFVDSLQDLMQVIEELFK ATTMMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNFLIISYTE AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIPVFVINY PLTLKPFYMRDNEDGPQELEGSVA*HSLGLMILLSIVVIGQP
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR NLVFLGIALTKPDLITCLEQGKEPWNIKRHEMVAKPPVICSHFP QDLWAEQDIKDSPQEAILKKYGKYGHANFQLQKGCKSVDECKVH KEHDNKLNQCLIPKKKK
5664	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE ETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR ANGHPQQNGEGEPVTLFEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFII GLFVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTLPFRM FYYAKDEWPFGEYFCQILGA
5667	1	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQ
5668	691	894	CSFLPCIPDLFLQPLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	1	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHPFFPK ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL NSQ
5670	3	373	SSECLTMAWIPLLLPLLILCTVSVASYRLAQPSSVSVSPGQTAK ITCSGDVLAKKYARWFQQKPGQAPVLVIYKDTERPSGIPERFSG STSGTTVTLTISGAQVEDEADYFCYSATDNFLWVF
5671	280	524	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
5672	2	557	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPAKDITGS SDPYCIVKVDNEPIIRTATVWKTLCPFNGEEYQVHLPPTFHAVA FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSP WPPSHSETSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS QAWLLLPLP
5673	327	696	ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGE AKNSITDSQMDDVEVVYTIDIQKYIPCYQLFSFYNSSGEVNEQA LKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQ DLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLG MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKIN EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID MFLKVAVTTTTISM
5675	80	753	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG KSGVPVSAPGSDGKWWEERPGMFSLMASCCGWFKRWREPVRKVT LLMVGLDNAGKTATAKGIQGEYPEDVAPTVGFSKINLRQGKFEV TIFDLGGGIRIRGIWKNYYAESYGVIFVVDSSDEERMEETKEAM

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			SEMLRHPRISGKPILVLANKQDKEGALGEADVIECLSLEKLVNE HKCL
5676	2	930	FVSSPPPRPVQPARPGGPGLSGRRSLLCQVASTPAHVGVMRSPV RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH HNQTGKKYQWDAETQGNILGSFFYGYIITQIPGGYVASKIGGKM LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN WTYVFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS L
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLWLIHH RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIQNSKRKGPEF TREFESVLVDAFSHVAREADEGCKKPLERLLNIWQERSVYGGEF IQQLKLSMEDSKSFPPKATEKKSLKRTFQQIQEEDDDYPGSY SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
5678	3	593	SSSPPSSTPSLPLPFYLLLGQLRLQLLMGTAHLSGAGEAAPCPG GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIEE SLAEFTEQFNQLHNRRNENLQLGPLGRDPPQRCSTFSPTDSGRE PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR AAALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE DDAEVQQECLHKPSTRDYIMEPSIFNTLKRYPQAGGSPENVIQL LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCL MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLQNRNSHTPLESLIHPQPSYKGFGIMFGKKKKKIE ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA RQTRPQRLRKRAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP PASCVFSQVMNMAAFLALVVAVLRFIQLKPKVLNPWLNISGLVA LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWIQAAL TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS QGPVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL QRIWGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGL PFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQ GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG LRHRSPGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEERSKGS ATYCTVCSKKPASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEEHDLC
5684	195	677	TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QSAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERIFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE RQLHMQLYPGWSARDNYVSPSSIPVALHS
5686	128	1181	CTNWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF

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			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGMP RMDFLINSSSGVVVTTTELDRERIAEYQLRVVASDAGTPTKSST STLTIHVLDVNDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN NDVGLNAELSYFITGGNVDGKPSVGYRDAVVRTVVGLDRETTAA YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIILQSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA QGDGGAAAVGHVLVVPAVGPVRVNPGLQTPVPRPELLPGP\SSS LHSDSSYPPDAGLSDDEPPDASLPPDPPPLTVP/ADA/PMPVT SGCRMPSTSASE/AAGCQGACTHAKGSETPPPASPQTSEPAPSP LPPHLTGGPGMYSSEAKLPNSFSCLGLAGTGAGI*GTASAHGTG PPVLPHVCTPSLANPQP\AVGPEASSLPLGVSGIGMSA/SAPIS SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP VLDI
5688	1	420	LTKWDLPGECYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLFP *SHMIIRSLL*KVIDDSLGQLPLLRELLL**LNVIDRCIILAYV LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID DGYIPAVF
5689	1504	3	HELSGKHISMVSGNTCNWHPGGHSPGGGGQGEITSKDRGEIPAL IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPPQPCEGPRSTSRG GEG*GHAVGPGREIGKEGSLPFLGPKALGP*SASCQRAFEGGAH GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQFWDQHPHS PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ KLFRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\ PQTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGGH GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLQCPCSK EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF GQELKGPLDAGRLWPGAPSASSSHR*GG*ERARAGAGHRGST*A SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P GSPPPA*ASAGRKGTVSTLGGGLL
5690	1424	58	PSPPAGVCAAPAPLPLLALARRDRRPCSPGAEAAPWQTGGPAID GAWRTSVSALRRGATG/APCSPGAEAAPWQTGGPAIDG\DGELP *VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGQGRQQDPEP DGLRHRQHGAASHARHRLQRLRPGHHQNRHVRRDPQAPPGGPAP GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERARPRH PTPQGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA*GNPQLE KAPRSDRNPSQGLRTRIRRPETPDCGPPSPAGSSASASTFRCTS SLSLLGP/PGAHNLDTAPQDR*HGP*GDKRGAPGVAGEDPRPP* GNFVR*LLLMP/GVA*RHGTSPELGPSLGENGGQWDSGNLPGTP KG*SHPAFTKST*SMEAEKSYWNHPHR\DRGRQGVRINCLRVGE SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTPFPPAG PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMDVSFSGILSPIRD VAHRMLATGRCTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG GVGVYVLLESVPLSYS
5692	1193	548	TQAWTRAEKDRKGSVRALRLHLRRGPPT*RGSHPL\QSVPCIQK PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQ RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLQS VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVETMGNGVD
5693	1258	1330	ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSQNTEPQAP *QAGPPSSLRPP\SRRR*APEWPKRATGSRCRGLSAPPWPWPAA RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS PEAIVWRSSRFPLWFPLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKPPPATGIATVMQTGGSATLSKIQKSSGIPV

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			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTQCI
5695	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTQCI
5696	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTQCI
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATRAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAKVAAPTKQPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLPGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA
5698	2	666	GARAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEENKPSRQTVPI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE FNQ
5699	2	1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG
5700	923	597	NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSPPPPTPNSARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD E*CSIASSLIKAILRVSVLSE
5701	59	410	IFEKICSDTQEFISPEINPQICSWLIFDKGAK/NHATGKDSLPN KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL LEENTGENLHDTGLGNVFLDMTPKTQPTKQK

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5702	3	1517	RTPVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR ASESSASSDGPHPVITPSRASESSASSDGLHPVITPSRASESSA SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGLH PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTN IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETLTMDI TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKP PTATPTTARTRPTT\A*VQVKNEVSSSCG*VWLPRKTSLTPEWQ KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAKR GCCP*PGPPPTDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
5703	14	1117	HHKDSRSQGLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA PKAGIGTKAKPSESHLKLHPGWPSLDRQGEPATLGTGTGHCSDS RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVQDKS**VSL DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR GSWETAPGS*WCPWL*AARWTGWRTASGASAGLGRAADRPSAWA RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA AGWPRHSPHDTQTPEP
5704	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPR QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE SPQP
5705	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE SPQP
5706	1161	610	QLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD DYVANTDNCSLKDLVRECRRYCAFNNWGSVEEQRQQQAELLAV IERLGREREGSFHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVPLLLCSI LFFIIFLF
5707	28	609	GSPAPTPGFRRRPGRGTPSPGTRHHQGRAEPEPDAPERAPLRR* MFAIQPGLAEGGQFLGDPPPGLCQPELQPDSKSNFMASAKDANE NWHGMPGRVEPILRRSSSESPSDNQAFQAPGSPEEGVRSPPEGA EIPGAEPEKMGGAGTVCSPLEDNGYASSSLSIDSRSSSPEPACG TPRGPGPPDPLLPSVAQA
5708	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSPSLGAPGAPSPL RVSPASGGPRKEGRQGSGG*AGGGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSGAGMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA PPPRPEPPPPPARRP
5709	2	2031	ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE

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			LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFM SNRFVETNLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK VLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVK MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT NPAIREQTVKSMLLLAPKLNRANLNVELMKHFARLQAKDEQGPI RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV LGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRS. FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAQQD DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA GAKLPGATS*RYTAGQRV
5710	1	562	IPGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK \LNGHDYMRNIVHLPVFLNSRGI./RQ/LQENFS*LQQQMETFHA QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV CIAIQFNTNKDDAT
5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFYPDSAQPFIVKSESS SQIAKAVLSQQRPSLFHECAFHFFS*SLQRHTINLDQGIP*LLM LSEERQHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL QIL
5712	3	1391	GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP ETVIDLINKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/ TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL HKIFHLW\DTLLLGEFLFPILYWE
5713	634	284	PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH TACRCSRRGAQVQHLPREDIRAAE*DPHLREVWPGLPTSSATSP *RAVLTSPCSHLGSADAASSHWLCGVSFH
5714	212	613	WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSSGPKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS HYSSPGSSGGSGGGSMMGGESADKATAAAAAASLLANGHDLAAA MA
5715	131	1979	ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQR QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHKHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWKVAAMLLLLRHGSHSEL TDLTEAQTSQH
5716	1711	1370	RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNLSFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT
5717	44	1489	LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD EGPGALVLESDLLLGQDLEFEEEEEEEEGDGNSDQLMGFERDSE

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			GDSLGARPGLPYGLSDDESGGGRALSAESEVEEPARGPGEARGE RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFV SHYSSHLKRHMQTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTG EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTP RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGQKLEEGEGSRLG AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYPNHLA RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGEKPYKCPL CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
5718	120	284	VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT S**STADPLHL
5719	48	428	ELNNGPFQNPLCNGGNLAVTGSWADRSPLHRAASQGRLLALRTL LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
5720	1	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK \RCT\YYE\TCGGTYGLQMWSVSPQDVAQKVVAL\RKKQQ\LAI GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE/SGGGSAFSD Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM QHPASG
5721	97	492	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA VFYAIAGGLPLERAYYYAFAAHITGITDTTRVGIILSRGTAASI SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
5722	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP QRSVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT KSSTREIPEMI
5723	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP QRSVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT KSSTREIPEMI
5724	3	1841	FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVAEEAADLDGEID LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTEKQEAELGEP DPEQKRSRARE\RRREGRSKTFDWAEFRPIQQALAQERVGGVGP ADTH\DPWRPEAEHGELERERARRREERKRKFGMLDATDGPGTR DAALRMEVDRSPGLPMSDLKTHNVHVEIEQRWHQVETTPLREEK QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSQKEASDLLEQ NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMKETHQKKIE DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME RELEKSQRSQISSVNSDVEALRRQYLEELQSVQRELEVLSEQYS QKCLENAHLAQALEAERQALRQCQRENQELNAHNQELNNRLAAE ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTQLC TQEPQGSAAWPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEQ
5725	3	1049	VNGHSEETSQSPNRTEPHDSDCSVDLGISKSTEDLSPQKSGPVG SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/PTSAVDG KNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA

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			LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFSNHN NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS SVSSTASVNLGDPGSTRRAQIPRGDYLSYREFHSAGRTPPMMPG SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR TSP
5726	2	486	SRSLSMWWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT GLIPHLGQARTPPYLQLQVTEKQVLLRADDG
5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDQASCEVLTVKKK AGAVTSTPNRNSSKRRSSLPNGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPGAPDPPAVE GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDWIPGPQGLWL HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED EPPQVPEAGEEDAVPAEEGPGGTPETQADQVRERPEAHLAEGGA KGSPRRLADPQDLPAGQMSLAPPFPPVAAVIRSNK
5729	1	1525	AGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKEPPGEL CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK QLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRV KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLP GPYHRGEAQRNIYRLINTAPGLVHLTAHSSLVCPLSLGGSLGLR PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLCSSPVS MVHL\ADMLSFCGKKVVTAGAIIPFPLAPGQSLPDSLMQFGGAT PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA LHACTTGERILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG
5730	1258	1713	KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT KIETEGFWERPRNFENQGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLRVA
5731	122	443	RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI EPSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRRQEWFFLRVY
5732	226	772	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKPLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA
5733	1	460	PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNANYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM
5734	3	968	RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL
5735	2	540	FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT
5736	1	382	GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV

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			TARLSVTPPNLLPTVSFPQPDLPDNPVYSTTTRKLASDLRANKN QES**ILPDSGIFIP*T*TSYLQSTTHLRRAKLPQLLRR
5737	290	1041	KACLHLLSSFLTSNFLFNPLLPDSLYSVEAR9QRANLGPCRRKR LQTLMRLAAGFQYSSHKDPSLSAKEKHTDYHNEARGPWPGWVG* RTADGSCGRGPDGAHHPGPKSSSWRASRLLPGLGGSHHLDAYVG RDLECGTPAPLQLEIPPQPRGHPAPIPTGQAGPRDSGPGASP*V ETRPLTDGRR*PGVRPVGWTPAHPAGTLRPRGAVEPSVSACGKW APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
5738	8	460	DTLSLNCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTYSNEV VTLWYRPPDILLGSTDYSTQIDMW*GQVEVWQGPCGKGGGLVTT ATQPAAFLFTVPSLPRGVGCIFYEMAIGRPLFPGSTVEEQLHFI FRILSEEAWALCAVETHR
5739	1	1222	SFQRRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC FPTLLEFLESLEPDLPALRAMGLELWAAGPGTHPAGISDLLAEV SAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI LQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATV VLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERG HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY TGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATS PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVAEVFEALDF LQEVNVYGVTV
5740	265	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A YVYERVYN*NISRMVHALEQKRHPAGLSSSMALQLNPCLGMLMA LQSELHKLYDEETQSWVSGSACGGYP
5741	1	650	PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK
5742	2	362	TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG
5743	2	415	GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREETPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE
5744	3	703	TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLPALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL
5745	1400	599	GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTR KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF
5746	3	821	SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER RATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV
5747	2	1328	DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE ESSSPVRKESSRGRHREKEDIKITKERTPESEEENVEWETNRDD

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			SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKE KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYQRTLTPPLRRS ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH ERRRDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR RE
5748	934	473	SEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEG KKNENLQNLLCGSGAGVISKTLTYPLDLFKKRLQVGGPRHARAA FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM FFSYEFFCNVFHCMNRTASQR
5749	552	1	GFPVDPRVRGSTLSLARRPKGMIRSGSFRDPTDDVHGSVLSLAS SASSTYSSAEERMQSEQIRKLRRELESSQRKVATLTSQLSANAN LVAAFEQSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN SRAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIQF ILEWAYVFLYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRF QENYVAQLILDVRREGDVLSNCEFTPAPTPQEHLTKNLELNDDT ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNNPVHTLTE VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL GCTSSALQIFEKLEYWE
5751	3	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ DVLQAIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPVKRRDREA LMASGSGGHNTMPSGGNSVSSGSSVSSCI
5752	3	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT VERFMELRHKNFMLRVETRARARAKAERENADIIREQIRLKASE HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV AERQHVGASWSPRSCPCRLCTAL
5753	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG GQEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEFAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW WPTPATPSPLTAPFSME
5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDRAQ DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDPCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA
5756	3	621	SSKIQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDPGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ LSISQSVHVAVKVPPLIQPFEPPPASIGQLLYIPCVVSSGDMPI RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI ASNAAATVSRRRQLIVRVPPRFVV
5758	1	474	FRRGAGAERGEHREGERGAAGMGEPKVHRVRFFNYVPSGIRCVA YNNQSNRLAVSRTDGTVEIYNLSANYFQEKPFPGHESRATEALC WAEGQRLFSAGLNGRIMEYDLQALNIKYAMDAPGGPIWSMAASP

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			SGSQLLVGCEDGSVKLFQITPDKIPV
5759	2	1240	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR MARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEWRNTF NKDVGADLVCYRRRGHNEMDEPMFTQPLMYKQIHRQVPVLKKYA DKLIAEGTVTLQEFEEEIAKYDRICEEAYGRSKDKKILHIKHWL DSPWPGFFNVDGEPKSMTCPATGIPEDMLTHIGSVASSVPLEDF KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL NGQDVERGTFSHRHHVLHDQEVDRRTCVPMNHLWPDQAPYTVCN SSLSEYGVLGFELGYAMASPNALVLWEAQFGDFHNTAQCIIDQF ISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSARPERFLQMSNDD SDAYPAFTKDFEVSQL
576C	1	1221	VRDITSDSLSLSWTVPEGQFDHFLVQFKNGDGQPKAVRVPGHED GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGQFDHF LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG QRVGPVSAIGVTAAEEETPTPTEPSMEAPEPPEEPLLGELTVTG SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPQVVRVGGEESEVT VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP TEPGTRAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR RLGPVSAIGVT
5761	3	1275	SCDMAEAAALVWIRSPGFGCKAVRCASGRCTVRDFIHRHCQDQN VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGFGSML RALGAQIEKTTNREACRDLSGRRLRDVNHEKAMAEWVKQQAERE AEKEQKRLERLQRKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK GMQAASSKMVSAEISENRKRQWPTKSQTDRGASAGKRRCFWLGM EGLETAEGSNSESSDDDSEEAPSTSGMGFHAPKIGSNGVEMAAK FPSGSQRARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK EHMESRMVTETEETQEKKAESKEPIEEEPTGAGLNKDKETEERT DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV AELELLGLEKLKCELMALGLKCGGTLQ
5762	2	344	GSTGQTPLHSQGGGGGSGGGRRRTPRGMPKEKYEPPDPRRMYTI MSSERAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKIR
5763	3	429	LDKDTGLIMLIARLDYELIQRFTLTIIARDGGGERTTGRVRINV LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL TVMAMDAGN
5764	19	441	VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAQRDKL
5765	3	825	QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGRATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGPGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKREEEEESHRRIKKLKTEKVDPLF TVPAPPPHV
5766	1608	663	SGLFSVDPASSQAMRLSDVTLIEGVGNKVMVVAGVVVLILALVL AMLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR
5767	2	892	NFRATPRPPTRPELRTGTEVILWYLDWRALMKRKRMKANIKLVG SGFPPLPSSDLDDSLTEKIDEKIGFRNDANFDWQNVADFRDAGGS LTEVKVEEEERDPQSPEFEIEEEEEMLSSVIPDSRRFNELPDFP

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			HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV NSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLQLEKDRLQ FLKFSSEKLQIEKERLQVEKDRLRIQKEGHLQ
5768	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPL SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN DRCVEVIAKEGQNLKELYLVSCKITDYALIAIGRYSMTIETVDV GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAGVNFAI AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT WEQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIQQPAMLLRE YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF LEGVGIREGGILTDSPGRIKRSMSSTSASAVRSYDGAAQRPEAQ AFHRLLADITHDIE
5772	148	383	EFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG ILTFSNLVTCSAIYHLPVFPERRPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS LRQYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPQHHKQLLL SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG RRLNISYTRNMTLKDGKNSK
5774	2	592	FVEEENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEKPDIFQLVSV KLPKSSSQRVEAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLWKGWDRKAQRNGL RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP RP
5776	2	484	RLPQDCVCQNLSESLGTLCPSKGLLPVPPDIDRRTVELRLGGNF IIHISRQDFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHL DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL EDLDLSYNNLHGPAVGLRGDANVQPSTS
5777	2	949	GQDPEPGQDLFQPERRVDPSWGRGREPRLGKLRFQNDHLSVLKQ VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKARAGSTLPENLG GGSGSRVSQRVHPSDLEGRRPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSERRNV
5778	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYRALV

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			PLPEEIQVSPGDTEIHRVEPEDVANHLTAFHWELPRCVHELEFV DYVFHGR
5779	138	1671	EAVQVLIKHSADVNARDKNWQTPLHVAAANKAVKCAEVIIPLLS SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR ALHWAAYMGHLDVVALLINHGAEVTCKDKKGYTPLHAAASNGQI NVVKHLLNLGVEIDEINVYGNTALHIACYNGQDAVVNELIDYGA NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTPLHVAARYGH ELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG QKYSIVSLPSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK EATLCLEFLLQNDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE RTNSGFEESDSGATKSPLHLAVSEMP
5780	154	624	QFFRVITCLPFKGPDYRLYKSEPELTTVAEVDESNGERKSEPVS EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM DLRTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHCQACLREK KKGLNVIGASDQSPLQSPSNLRDNP
5781	19	941	RGSLGGHPWRPPMRAASQGCLPVSFVTGPHQERAYGGRGPGGAF PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ VQPHFTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT QHSIHTVTCKSPRQKEDRSPKPPQAPKHPERHGRQS\QAPPPLP VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY NIMD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVAREHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSKHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSRS/RDRRRRSSRSRSKSRGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEEEEPPFYHHPFKLSEPKPIFPNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGERN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAPDLEAMSM LNRAQERIDAWAQLNSIPCQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKNGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y
5783	1693	698	DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL NDLIEE/PI*SQ/PKILPQQP/LILKVALNMARGLKYLHQEKKL

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			LHGDIKSSNVVIKGDFETIKICDVGVSLPLDENMTVTDPEACYI GTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLSIPHINLS NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIE LFSVCTNEDPKDRPSAAHIVEALETDV
5784	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5785	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5786	2532	1674	SYKLPAAERRASSCSQPPTPTRRRWPAPGRTSRGHRPQM*SGTP APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKRFPRNWNPMMAE
5787	2	1460	MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKERERIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QDGDILRQRDEPDLLVAGEICRPSALIEELEEKNERPARELLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQPSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS
5788	2	6860	EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS TETLQCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDPF

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			LCNACGFCKYARFDFMLYAKPCCAVDPIENEEDRKKAVSNINTL LDKADRVYHQLMGHRPQLENLLCKVNEAAPEKPQDDSGTAGGIS STSASVNRYILQLAQEYCGDCKNSFDELSKIIQKVPASRKELLE YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRRGA AAMREEVRQLMCLLTRDNPEATQQMNDLIIGKVSTALKGHWANP DLASSLQYEMLLLTDSISKEDSCWELRLRCALSLFLMAVNIKTP VVVENITLMCLRILQKLIKPPAPTSKKNKDVPVEALTTVKPYCN EIHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSELRH LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFTPAT QAARQAACTIVEALATIPSRKQQVLDLLTSYLDELSIAGECAAE YLALYQKLTSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA TLSTDLQQGYALKSLTGLLSSFVEVESIKRHPKSRLVGTVLNGY LCLRKLVVQRTKLIDETQDMLLEMLEDMTTGTESETKAFMAVCI ETAKRYNLDDYRTPVFIFERLCSIIYPEENEVTEFFVTLEKDPQ QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICQDCDLVALLED DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEPMRIVYRMRG LLGDATEEFIESLDSTTDEEDEEEVYKMAGVMAQCGGLECMLN RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNRQQLVKLEMNTLN VMLGTLNLALVAEQESKDSGGAAVAEQVLSIMEI\IQAEPNVEP LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLLRIIP YLSFGEVEKMQILVERFKPYCNFDKYDEDHSGDDKVFL\DCFCK IAAGIK\NNSNGHQL\KDL\ILQKGITQNALD\YMKKHIP/SAA RIWDADI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI PNLHKLEQVS\SDEGIGTLA\ENL\LESLREHPDVNKKIDA\AR RETRAEKKRMAMAMRQKALGTLG\MTTNEKGQVVD/TRTALLEA DWEELIEEP\GLTCCICREGYKFQPTKVLGIYTFTKRVVLGGVW ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREEWESAA LQNANTKCNGLLPVWGPHVPESAFATCLARHNTYLQECTGQREP TYQLNIHDIKLLFLRFAMEQSFSADTGGGGRESNIHLIPYIIHT GLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFTV LALHILPPEQWRATRVEILRRLLVTSQARAVAPGGATRLTDKAV KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLAEYIR HNDMPIYEAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE SFLKDLLNSVP
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ TEEKEKKEKPKSDKTEEIAEEEETVPPKAKQVKKKAEPSEVDMN SPKSKKAKK\KEEPSQNDISPKTKSLRKKKKEPIEKKVVSSKTKK VTKNEEPSEEEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP EPDCNPSEAASEESNSEIEQEIPVEQKEG\APSNFPISEETIKL LKGRGVTPLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL IEKLHG\ELQDRERGRAPQVLVLAPTRELANQVSKDFSDITKKL SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWVFNVAKKYMKSTYEQVDLIGKETQKTAITVEHLAIKCH WTQRAAVIGDVIRVYSGHQGRTIIFCRTKKEAQELSQNSAIKQD AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLEGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ
5790	3786	1585	ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEEESESEDSEDSGGEEE DAEEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTPKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN HVSFCYLIVLMRNRMETVEDTNGSETGFRAWNVQSRGRIFLVSK

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			PVLQQINTVDVLTTMGAIPAGFRPSTLSQLLEEGNQFRANYFLQ PELMPSQLAFRDLMWDATEGTIRSRPSRISLILTLWSCKMIPLP GMSIQVLSRHVRLCLFDGNKVLSNIHTVRATWQPKKPKTWTFSP QVTRILPCLLDGDCFIRSNSASPDLGILFELGISYIRNSTGERG ELSCGWVFLKLFDASGVPIPAKTYELFLNGGTPYEKGIEVDPSI SRRAHGSVFYQIMTMRRQPQLLVKLRSLNRRSRNVLSLLPETLI GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLISHPMLATFPML LEQPDVMDALRSSWAGQES\TLKRSEKR\PKEFLKVPRFLLVYH \GCVLPLL/HTPTRLPPFRWAEEETETARWKVITDFLKQNQENQ GALQALLSPDGVHEPFDLSEQTYDFLGEMRKNAV
5791	3	1636	LRVAEFAGTSR/IGAGLIQPLHRAPARDHGLCRGGAAPALSVSH GN/GKQL/AMSSQGSDDEQIKRENIRSLTMSGHVGFESLPDQLV NRSIQQGFCFNILCVGETGIGKSTLIDTLFNTNFEDYESSHFCP NVKLKAQTYELQESNVQLKLTIVNTVGFGDQINKEESYQPIVDY IDAQFEAYLQEELKIKRSLFTYHDSRIHVCLYFISPTGHSLKTL DLLTMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLNSELVSNG VQIYQFPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGNKMVKA RQYPWGVVQVENENHCDFVKLREMLICTNMEDLREQTHTRHYEL YRRCKLREMGFTDVGPENKPVSVQETYEAKRHEFHGERQRKEEE MKQMFVQRVKEKEAILKEAERELQAKFEHLKRLHQEERMKLEEK RRLLEEEIIAFSKKKATSEIFHSQSFLATGSNLRKDKDRKNSQF FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVICFITSIFGEQPQ LLIFMEKYFQVQGQYISQSE
5792	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLPLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQPGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLPMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD
5793	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLPLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQPGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLPMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD
5794	1	5016	MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG PPGEIGFPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK

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			GEPGEFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG PKGSPGSVGLKGERGPPGGVGFPGSRGDTGPPGPPGYGPAGPIG DKGQAGFPGGPGSPGLPGPKGEPGKIVPLPGPPGAERGLPGSPGF PGPQGDRGFPGTPGR\PGL\PGEKGAVG\QPGIGFPGPPGPKGV DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL PGLPGIPGTPGEKGSIGVPGVPGEHGAIGPPGLQGIRGEPGPPG LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGEKGFPG FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFPG SKGEMGVMGTPGQPGSPGPWGAPGLPGEKGD\HGPPGSSGPRGD PGLKGDKGDVGLPGKPGSMDKVYMGSMKGQKGDQGEKGQIGPIG EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP GPKGSVGGMGLPGTPGEKGVPGIPGPQGSPGLPGDKGAKGEKGQ AGPPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDGIPGVKGEAGLPG TPGPTGPAGQKGEPGSDGIPGSAGEKGEPGLPGRGFPGFPGAKG DKGSKGEVGFPGLAGSPGIPGSKGEQGFMGPPGPQGQPGLPGSP GHATEGPKGDRGPQGQPGLPGLPGPMGPPGLPGIDGVKGDKGNP GWPGAPGVPGPKGDPGFQGMPGIGGSPGITGSKGDMGPPGVPGF QGPKGLPGLQGIKGDQGDQGVPGAKGLPGPPGPPGPYDIIKGEP GLPGPEGPPGLKGLQGLPGPKGQQGVTGLVGIPGPPGIPGFDGA PGQKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFL VTRHSQTIDDPQCPSGTKILYHGYSLLYVQGNERAHGQDLGTAG SCLRKFSTMPFLFCNINNVCNFASRNDYSYWLSTPEPMPMSMAP ITGENIRPFISRCAVCEAPAMVMAVHSQTIQIPPCPSGWSSLWI GYSFVMHTSAGAEGSGQALASPGSCLEEFRSAPFIECHGRGTCN YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR RT
5795	1192	61	STRSPTVEYISAHPHILEMLLKGYEAPQIALRCGIMLRECIRHR PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR
5796	2	1078	GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF PGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG
5797	2	891	PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQRANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIERANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQIQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
5798	644	115	KILGSRWKSNSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
5799	2679	1435	LLSTYIKFINLPPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLERKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNPSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRPRYGGAPQALTLKLPVTINKFFQPTEM AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA

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			LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL RTSKEPVSRHLCELLAQQF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL RTSKEPVSRHLCELLAQQF
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQP CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE QLGIKLVRKVDEPGVPIFNVLDGGVAYRHGQLEENDRVLAINGH DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS NGSNSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT KVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH NMAPPSDWSPSWVMWLRLPRCLYNCKDIVLRRNTAGSLGFCIVG GYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMERIMDLPTLLRHAFREMPSVGGLFWMFRIRIILCLM GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLLIYISIMYREV ITQRLTR
5803	2234	1299	RAQFGTTARIYAYREEQDFGIEIVKVKAIGRQRFKVLELRTQSD GIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICA SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI LCL
5804	2	1707	EMEKQRQEEQRKRTEEERKRRIEQDMLEKRKIQRELAKRAEQIE DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNPEDLEKE REEKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIESEAKK ESLSPGKLKLTFEELERQRQENRKKQAEEEARKRLEEEKRAPEE ARRQMVNEDEENQDTAKIFKGYRPGKLKLSFEEMERQRREDEKR KAEEEARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP GKLEINFEELLKQKMEEEKRRTEEERKHKLENEKQEFEQLRQEM GKEEEENETFGLSREYERLIKLKRSGSIQAKNLKSKFEKIGQLS EKEIQKKIEEERARRRAIDLRIKEREAENFHREDDVDVRPARKS EAPFTHKVNMKARFEQMAKAREEEEQRRIREQKLLRMQFEQREI DAALQKKREEEEEEGSIMNGSTAEDEEQTRSGAPWFKKPLKNT SVVDSEPVRFTVKVTGEPKPEITWWFEGEILQDGEDYQYIERGE TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLARHASS APKESQQQSEDREYEVKERLYPKSKRRYDTYNIAGYQGEIEVGL YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA LRNYIPYLTKLKPSLKKSFDPFDEYFVLLKPRNNIKQNEEAKTR RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSEPLQVERCRRNLV ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	AVPTFHNHGRTANLYSLHSNLGITTVFLFACQRFLGFAVFLLPW ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	RFSKKTFRRPMAVDIQPACLGLYCGKTLLPKNGSTRIYGRCGVC PRGQRTNAQKYCQPCTESPELYDWLYLGFMAMLPLVLHWFFIEW YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV

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			LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQAVGG GLLYYAFPYIILVLSLVTLAVYMSASEIENCYDLLVRKKRLIVL FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT EPSRILSEGANGH
5808	2	433	SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKNGSS EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTHMNV LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP LVNGVHLPNRR
5809	464	2422	ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWQ INSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVC LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHATSFN FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPA VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGQRWYQKEF AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSRLPVVISL TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQVLV LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM RIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV
5810	3	1641	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIEAFVS EIESFFNTIEENCSKNEKRLEEQNEEMMKKVLAQYDEKAQSFEE VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDQMLK QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME EPQDDQEVNELVEEYRLTVKESYCIFEDLEPDRCYQVWVMAVNF TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPEA TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLQPNDNYFFYV RAINAFGTSEQSEAALISTRGTRPLLLRETAHPALHISSSGTVI SFGERRRLTEIPSVLGEELPSCGQHYWETTVTDCPAYRLGICSS SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR VGLLLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALEKPG KCTLHLGIEPPDSVRHK
5811	1918	851	AAALADPLPEDKWSAEKRRPLKSSLGYEYTFSLLNPDPKSHDVY WDIEGAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDS ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD
5812	5204	2744	GGRQRCQRGRSCGAREEEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHEEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS QRLQRSLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPQ GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDNVH AAELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS EERLLEEGVLRQIPVVGSVLNNFSPVQALQKGRTFNLTAGSLES

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			TEPIYVYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSLRGSDA LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH TDQTEAFQKGVPHPEDDHSQVEGPESLR
5813	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI GCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFT RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLRDENETKVI KQCYQDHNLSQNGSAPTFPLCAMQLPSHMAWLSFSTAT\CMRRS SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVA ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL PRNVMFVFFQGETFDYSGSSRMVYDMEKGKFPVQLENVDSFVEL GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP AVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYY QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS ILQGRDLRSYLG*RGLFQH\YIAV\SSPTNTIYV/VLQYALANL TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP RCVRSTARLARALSPAPELSQWSSTEYSTWTESRWKDIRARIFL IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA VSY
5814	8500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLNSRRESL GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVYEA\I AAPIIDSAIQGYNGTIFA\YGQT\ASGKTYTMMGSEDHLGVIPQ GQFHGHFSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTQKM KPLIIREDVNRNVYVADLTEEVVYTSEMALKWITKGEKSRHYGE TKMNQRSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLQQEL KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LRRIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK KDQRMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKKMQVDLEKRLQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKKVEENEALRREVILLSELKSLPSEVERLRKEIQD KSEELIHITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQREQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQRSHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LRAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEER KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH

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			QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR IAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEK IQELKANEHQLITLKKDVNETQKKVSEMEQLKKQIKDQSLTLSK LEIENLNLAQKLHENLREMKSVMKERDNLRRVEETLKLERDQLK ESLQETKARDLEIQQELKTARMLSKEEKETVDKLREKISEKTIQ ISDIQKDLDKSKDRLQKKIQELQKKELQLLRVKEDVNMSHKKIN EMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDE LRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQ HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH RIMKKLKYVLSYVTKIKEEQHECINKFEMDFIDEVEKQKELLIK IQHLQQDCDVPSRELRDLKLNQNMDLHIEEILKDFSESEFPSIK TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV NNFFNNRIEAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF KNYQTLKTSLASGAQVNPTTQDNKNPHVTSRATQLTTEKIRELE NSLHEAKESAMHKESKIIKMQKELEVTNDIIAKLQAKVHESNKC LEKTKETIQVLQDKVALGAKPYKEEIEDLKMKLGKIDLEKMKNA KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN EQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK SPEVTGTASKKKQITPSQCKERNLQDPVPKESPKSCFFDSRSKS LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK DVP\ECKTQ
5815	23	1460	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE QNCTLEIESYGYTTDDIEFYWNGGDGAVTGVNKIELPQFSIVDY KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL SWVSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDPKA TMYSYDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRIRRRAS\ QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
5816	861	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP TVYHERQRLELCAVHALNNVLQQQLFSQEAADEICKRLAPDSRL NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ VLGLILNLPSPVSLGLLSLPLRRRHLRWPCARL/VTVSYYNLDS K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG SWLRTD
5817	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVQK KKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLSP GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA HPQALMGRGFPSGMAAAGRHLCFL
5818	3	3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD DRRLGKKPIFSSSQQRKQVSDSGDIKIKSWRGNNKKECWSYLST NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA TAAAAATGQKNLLNGKGVRNQEGQISGARPKVLTGNLNVQAKAK PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECLDEPKENGS TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH DVRDNNNKDSVSEQKPHKPLINLASEISDAEALQSSCRP\DPQK PLNDQEKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVSDVS LCNPERTNGTLNSAQRDKKSKVPVEGLTIPSKLSDRSAMDEDKH

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			ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSQDDD GSNDRGISKCGTMLCHDPLGRSSSDTSTPEELKIYDSNLRIEVK MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQPQ GIINLAFEDATENKCREFSANKKFKRSVLLSVDECEELGSDEGE VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE CKQNKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL DLHQRRPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESHSTTTEK ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFEQ KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV PEDLSLAQYLINQTLLLARDSSKPQGITHIDTLNRWSELTSPLD SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLLGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGL LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMP KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFQNRKILPGGNT SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHL ELPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK TNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPKV LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN NILLITNASKFHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG KKSKIANIYFDPGLQCGDHCYVGLPPLSKSEPKVQPGVAMQEDM WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI TAELSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHIETIE ISGYSCEGYGFKVVNCQEPTLSANASRDIIILFTPDFTASRVIR ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWKLALYII ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPPD VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH SSEDSDITSLIEAMDKDFDHHDSPALEVFTEQPPSPLPKSKGKG KPLGREVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGPSSSLGIS HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSWPAS SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR RSSDPWSNSHFPHRN
5820	310	1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEPEEKMN ENWKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\ SSSSDSSSSSSDSEDEDKKQGKRRKKKKNRSHKSSESSMSETES

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			DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS ESEYIEEVRAKKKKSSEEREKATEKTKKKKKHKKHSKKKKKKAA SSSPDSP*H*EKSGFPYKESAMSEEISTVKITTYLLKCMNFLVF GIIPGLFSSHSDATV
5821	179	915	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT PT/IKDCSIAATGKRPSARFPHQRRKKRRRMDDGLAEGGPQRSN TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\ SRIPSPLAALRMQGTP*RWSPFEPEPSPSTLIYRNMQRWKRIRQ RWKEASHRNQLRYSESMKILREMYERQ
5822	464	4379	QTLKEMPIVMARDLEETASSSEDEEVISQEDHPCIMWTGGCRRI PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHFPRSYE LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLLPAEYAEFCNSYS KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY LKQEGRDTTALMAHVEDLIIKTIISAELAIATACKTFVPHRSSC FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD MFTVVGFVCQDPAQRASTRPIYPTFESSRRNDFQKPQRCRPLSA SDAEMKNLVGSAREKGPGKLGGSVLGLSMEEIKVLRRVKEENDR RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG APELKI*SLNSKAKLHAALYERKLLSLEVRKRRRRSSRLRAMRP KYPVITQPAEMNVKTETESEREEEVALDNEDEEQEASQEESAGF LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL LERTRILAHQLGDFIIVYNKETEQMAEKKSKKKVEREEEDGVNM ENFQEFIRQASEAELEEVLTFYTQKNKSASVFLGTHSKISKNNN NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSDKLSRFTTSA EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP RCRSGSHTIGPFSSFQSAAHIYSQKLSRPSSAKAGSCYLNKHHS GIAKTQKEGEDASLYSKRYNQSMVTARLQRLAEKQAARQYSPSS HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ SDPQAPENHSSSPGSRSLQTGGFAWEGEVRNNVYSQATGVVPQH KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQAIFGSQT LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAFVP ITSSTDPAHTKIMNHKHTEKQPVHHSWVHD
5823	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA L\PAGPVG\ASSNQAKRVDVSELAAEQLTAPP\SASPTQPQTPE GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR GSPPSRVPQALNFSPEESDSTFSKSTATEVARREAKPGGDAAPS EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK ENVDSPLLKF
5824	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP

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			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK ENVDSPLLKF
5825	2	4210	FLQIESASPAPFSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAAGALERSFVEL SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGFYYVESG KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFQNCS VLPGGVYVSETQNRVI:LMLTNQTVHRLLLPHPSRMYRSEIVVD SQMQSIFTDIGKVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD GRALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCQDHKLRMWS YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYL GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPER EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL DLSWSELKKEVTLAVENELQGSVTEYEFSQEEFRNLQQEFWCKF YACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLVD HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV DMSVIMEMSCYNLQSPEKAAEQILEDMITIDVENVMEDICSKLQ EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTQLY GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESN LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL FSQPKAPLSQTGLNWPEMITAITSYLLQLLWPSNPGCLFLECLM GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL ECFCQAASEVGKEEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLD VIGLPELVIQLATSAITEASDDW\KSQATL\RTCIFKHHL\DLG \HNSQAYGSL*PQIPDSSRQLDCLRQLVVVLCERSQLQDLVEFS YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG TVMFEYGMRLGREVRTLRGLEKDGNCYLAALNCLRLIREEYAWI VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE CSLARIRLTLAQHDPSAVAVAGSSSAEEMVTLLVQAGLFDTAIS LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAQARAWAWLAANQLS SVITTKESSATDRAWRLLSTYLERYKVQNNLYHHCVINKLLSHG VPLPNWLINSYKKVDAARLLRLYLNYDLLDLTPYQVIRICGC
5826	3	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIQSLQAELAW WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPQGQHG CREQLELFQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLSALQPSLTAQTA PPQPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT WQGLVVDPSPHPLLAFPLLSSAQVHF
5827	194	2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK RENEDKVNKAAKVP**HLKTLRHPCLLRFLSCTVEADGIHLVTE RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL SSVFVSRDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP EEMSPEFTTLPECHGHARDAFSFGTLVRSLLTILNEQVSADVLS SFQQTLHSTLLNPIPKNRPALCTLLSHDFFRNDFLEVVNFLKSL TLKSEEEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP

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			VAV\KSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLF EVHEEHVRMVLLSHIEAYVGALSLREQLKKV\IL\PQVLLG\LR D\TSDSIVAITLHSLAVLVSLLGPEVVVGGERTKIFKRTAP\SF TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKK SEEWPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV EESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL GLGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRT EMVPKKDDVSPVMQFSSKFAAAEITEGRAEGWEEEGELNWEDNN W
5828	2	257	AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQAVV MAVGGGSRMTDLTSSIPKPLLPVGNKPLIWYPLNLLERVGFEEV IVVTTRDVQKALCAEFKMKMKPDIVCIPDDADMGTADSLRYIYP KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMLMRKGQDSI EPVPGQKGKKKAVEQRDPIGVDSTGKRLLFMANEADLDEELVIK GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS RL\IPYLV/RGKQFSSASSQQGTRKEKEGGSKGKRGLKSFRISY SFY*KEANYTGTGAPY\D\ACWI
5829	260	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGGELF ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY PRTPHPHEEKVETVEDFFLHLLRLIQSLR*SICRSLLPLLWISF LLILPQQQKPVVGLCQCRVKRPVDIS*TLP*CHQNVCQQPRKRK QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILEQR LTLTEDKLKDCLENQQKLFSAVQQKS
5830	4496	3139	GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNW NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR PQPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRPDPRSRV TDPVGDIVSFMHSPEEKYGRAHPVFYQGTYSQALNDAKRELRFL LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPE GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPDDL INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLR ADQEKERKKRERERERKRRKKEEVQQQKLAEERRRQNLQEEKERK LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHPSQSLTVIHDF LPSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQE\A GLSHTEVLFVQDLTDE
5831	71	2897	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQVKD TDDIESPKRSIRDSGYIDCWDSERRSDSLSPPRHGRDDSFDSLDS FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAERREYR KSWSTATSPAGLGKKALQDYGPRT\PVS\DDARSTSMFDMRCSE EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKREERKKMEKLLAGEDGTSERRKSIKTYREIVQEKERRE RELHEAYKNARSQEEARGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMPEGVARVH GSPLELKQDNGSIEINIKKPNSVPQELAATTRKTEPNSQEDKND GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND VSEEKDQKKPENEMSGKVRLVLSQKVVKPKSPEPEATLTFPFLD KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEKRRR QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEKEERRY YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDEKQDRRWKKSPQGDDSDLLLKTRESDRLEEKGSLTEGAL AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL
5832	2454	829	PGRRPRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN SENLRKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF

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			VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH RVHFHLPYRWQFLDRGKWEDLDNMELIREAYCNPKIERILCSES ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP QDVTTMQTCNTKFFGPKSIPDYWDSSALPDPGPQKITLSSSSEE YQKVWNNLFNRTLPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF ARDAAYSHHYSXSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV TPSILLALGSLFSSRQ
5833	170	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR GRDWNVKWEENLLHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF RNRELEATRRQRMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRLKDDEIL KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM KKAASKGLEQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EE\MGN PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLES VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDSTEH SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH SALIYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT STASPAVTPAADASDQDQPTVTNNPEPRG
5834	17	4020	RFRRGGGRVPPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLKEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSRAYLITLGKFINMPAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLEVISGYEELLADIVNLCVDYYENRMYLTPSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQNSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDPSQ VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPPNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSQEFQRDKQPNAQP QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV MEELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE EVCDLLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP

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			LIERLGTPQQIAIAREGDLLTKERLCCGLSMFEVILTRIRSFLD DPIWRGPLPSNGVMHVDECVEFHRLWSAMQFVYCIPVGTHEFTV EQCFGDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDGKD EIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGEGTPVE HVRCFQPPIHQSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPEVVVSRCMLQNNNNL DACCAVLSQESTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLQ SQNIYHHGREGSRMNGSRTLTHSISDGQLQGGQSNSELFQQEPQ TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLCSKGTSSLSQQT PRFNPIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPQGNSIYI RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS SQSSAHSQYNIQNISTGPRKNQIEIKLEPPQRNNSSKLRSSGPR TSSTSSSVNSQTLNRNQPTVYIAASPPNTDELMSRSQPKVYISA NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP GVVSPTFELTNLLN:PDHYVETENIHHLTDPTLAHVDRISETRK LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A QEFETSWGNIWRLRLYRRF*NYAGMVAHTCSPSYSVD*ALLVHQ KARMERLQRELEIQKKKLDKLKSEVNEMENNLTRRRLKRSNSIS QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTEDDEGAQWNCTA CTFLNHPALIRCEQCEMPRHF
5836	361	2303	FHITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK SDVNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGEIFSGIK VEAEENDTQILFNYLSSCKNESEILSLFSEVQGPWSFIYYQASS HYLWFGRDPFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE VPAS\DFSELILSLLSFPDALFYNCILGNIFLGRILLKKMLIA* VKFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEEKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIEKETKL
5837	4792	903	NGNAVAQAPVTNCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAPSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTRISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCFPIDGYSPGCWD\AFPGKEAPVAIPRG\HQGRLLCVAWSPL DPDCIYSG\ADDPCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEEQARRPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEQY QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW

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			DEAVQALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD HQSPATPAFKSLEAFFLYGRLYEFWWSLSRPCPNSSVWVRAGHR TLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM LSTPKELFSEKHASLQNSQRTVAEVQETLAEMIRQHQKSQLCKS TANGPDKNEPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRLTE ANQRMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMQQ QAQELLQKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDFSQEEWECLDPAQRDLYRDVMLENYSNL ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNG LGDNMECKGNLEGQVSKSEGLYMCVKITCEEKATESHSTSSTFH RII/HYQGKIVKCKECRQGFSYLSCLIQHRENHNI*KCSEVNKH RNTFSKKPSYI*HQ\KFRLGEKPYECMECGKAFGRTSDLIQHQK IHTNEKPYQCNACGKAFIRGSQLTEHQRVHTGEKPYDCKKCGKA FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG EKPYECKECGKAFILGSHLTYHQRVHTGEKPYICKECGKAFLCA SQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERPY KCKECGKAFISNSNLIQHQRIHTGEKPYKCKECGKAFICGKQLS EHQRIHTGEKPFECKECGKAFIRVAYLTQHEKIHGEKHYECKEC GKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHQ RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRTHTGEKPYECKEC GRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRL HN*EYSSHKICMHSIALASLDFAHLQEKNPEN
5839	1	2425	GRPFPRPPRALPRLPLRGRRQDGRWTVDFEECLKD\SPRFRAAL EEVEGDVAELELKL\DKLVKLCIA\MIDTGKAFCVANKQFMNGI RD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L*PNS EIN*GHSFQNFVKEDLRKFKDAKKQFENSQ*KRKKIALVKNAPV PSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSE ILKSMLSFMYAHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGDA AKEKREMEQKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFK RASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVK HCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT AYREKDDESEKLDKKSSPSTGSLDSGNESKEKLLKGESALQRVQ CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSK VRSLTLDTWEPELLKLMCELGNDVINRVYEANVEKMGIKKPQPG QRQEKEAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSE EKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRESLPS TVSANSLYEPEGERQDSSMFLDSKHLNPGLQLYRASYEKNLPKM AEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFLLQNGAN VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEEGKDP LSIAVEAANADIVTLLRLARMNEEMRESEGLYGQPGDETYQDIF RDFSQMASNNPEKLNRFQQDSQKF
5840	698	3610	KHLHLPRQHLTTLWQISSPRWRSPQRAFMSALSKTQTQSAPALQ GLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSS AQPFIPKSFNYSPNSSTSEVSSTSASKASIGQSPGLPSTAFKLP SNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL \EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFQ RGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSVDTMSLL SKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPPGLGSE SPYKQPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP PPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSYSHRAQEFGV KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS LFSPQNTLAAPTGHPPTSGVEKVLASTISTTSTIEPKNMLKNAS RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQEEHY RIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQT VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA SLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH LPPSPLEHGTPFQREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLSNPFTKEAALAHAAPPPPPGEHSGIPFPTPPPPPPPGKHSS SGGSGVPFSTPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP KDHSSLLQGTLAEHFGVLPGPRDHGGPTQRDLNGPGLSRVRESL

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			TLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDTISRSGIT LRSPRPDFRPREPPLSRDPFHSLKRPRPPFARGPPFFAPKRPFF PPRY
5841	1908	762	GLRLFLVLTVWPMMKPSWLSRTEPSKRLLCRTLWCQSGWSSRSY TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW RHCWMTARSCSGEKGGHWAFRQVGVYLLPGRVGCVSSRVSPSFP GDGLDSGLARRGSAVSALASGLVEEPMLGPPFHPTPRFKAVSAK SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND QSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQ\QE \VEPMCKESDHIHIIALAQGLQRVHPGWEYMGPRPRAATTNPHI FP*GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA LGHCYRGFSVVVKWSYFTPFFLSHDPPPMFY
5842	307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL WSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHCQAAEKGP HRSRDTAEPSFPEIPLDGTLAPPESQGNGSTLQPNVVYITLRSK RSKPANIRGTVKPKRRKKHAVASAAPGQEALVGPSLQPQEA\EG KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLQPSS RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA RLLVLEGGAPGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRILGL NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTW GTYQQLLKQKCWQNGRVPKPESGCTEIHHHEWSKMALFDFLLQI YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH DPRHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQH LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN AHGVKVLPMNE
5843	500	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGM RGSRMSQPPQCLRRAQSSCCHFMVKLLDDGTFMIPGEKVAHTSL DALVTFHQQKPIEPRRELLTQPCRQKDPANVDYEDLFLYSNAVA EEAACPVSAPEEASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCELVVT LGCPRIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP LTAPGTKRQKGPHQEGREVGQLH*GDPRGQELAPNGSESPILPG VQARAPGLGRA
5844	202	2471	FDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHL QYGKEYPHLPQYMKEIQPAPRMGKRAVPKKGKEIPLASLRGEQG PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGRIGPMGIP*PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGPGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGL PGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAKLTAPFPPVGAPVKFNKLLYNGRQNY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS SFSGYLLYPM
5845	215	2061	HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER GPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP KPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK PFPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNEFFGEGKT RQAARHNAAMKALQALQNEPIPERSPQNGESGKDMDDDKDANKS EISLVFEIALKRNMPVSFEVIKESGPPHMKSPVTRVSVGEFSAE GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HPFKKRPKT IVKAGPEYGQGMNPISRLAQIQQAKKEKEPDYVLLSERGMPRRR EPVMQVKVGNEVATGTGPNKKIAKKNAAEAMLLQLGYKASTNLQ DQLEKTGRNKGWSGPKPGFPEPTNNTPKGILHLSPDVYQEMEAS

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			RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC DRQSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLEKSKLFALG N.
5846	1126	456	FSKLIMKTPIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK LQGVI
5847	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPEVIVEK EKRDDSWSSNLLESWEYEGSLERQQANQQTLPKEIKVTEKTIPS WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK KEKSCKCNECGKAFSYCSALIRHQRTHTGEKPYKCN*/CVEKAF SRSENLINHQRIHTGDKPYKCDQCGKGFIEGPSLTQHQRIHTGE KPYKCDECGKAFSQRTHLVQHQRIHTGEKPYTCNECGKAFSQRG HFMEHQKIHTGEKPFKCDECDKTPTRSTHLTQHQKIHTGEKTYK CNECGKAFNGPSTFIRHHMIHTGEKPYECNECGKAFSQHSNLTQ HQKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYKCNEC GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNQHQKT HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYQCHECGKTF SYGSSLIQHRKIHTGERPYKCNECGRAFNQNIHLTQHKRIHTGA KPYECAECGKAFRHCSSLAQHQKTHTEEKPYQCNKCEKTFSQSS HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQENPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*PCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLLHSKFHL CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSXEAV SQRLCELLSAQF
5849	3545	1895	KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTREDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHRRDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLPGPLTRPPHNWMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LSKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE CRLSRRQYAEQELEQVRMALKKAEKEFELRSSWSVPDALQKWLQ LTHEVEVQYYNIKRQNAEMQLAIARDEAEKIKKKRSTVPGTLHV

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			AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWQQIEKICGFQ IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT PPIVSQFPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA PHAPHPSHPRHPHHPQHTPHSLPSPDPDILSVSSCPALYRNEEE EEAIYPSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN IIS/DERYQEMRCP*RIPSGGIL
5850	3	1895	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVPCE SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN QFILELFHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA NSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG NILAAVYAKMMGIPIRKFICASNQNHVWTDFIKTG\HYDLRGKE N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDSQLMTRLFNRLES QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPAIMQALKIKEI NETSSSQLYLLGSYNALPPLHEALLERTKQQEKMEYQVCAADMN VLKSHVEQLVQNQFI
5851	3120	1802	RCYLQFLALLLTSTSARAAAAIAAAEEPAGSPSVMTRAGDHNRQ RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELY GNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVV QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI ANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNI LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH ELEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	1	422	KTTFPSSLCPLRQLPEVRGYSGQPLTDPLISLCRSHKCRGKGWG SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGPPITSGPG/WFRQ YYFFISGRH*VLPTESDFYYVAMDFGGHGLSSHYSPGVPYYLQT FVSRIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRNP ESGAWALAPGLPAIHGRSWES
5853	223	1346	RLLGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FPIPRP LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESE SRWVRGNFRTGTAATLIGFSRNPTLNGSENWGSLVSIQEEGPDT GWEREKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE LXHLCAMIKRVLLERLENTRKLRELTEGRTLDWPQNRITEVSAK RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS GAETIKDLLE/ENFPELKNELDLQMEKAHRIPLKFNEKKAASRH IRVTFL/KFQRRNILQASSQRKQVTYKGAKVRLTSDFSPAILNA RRQW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG LGKYINQELSLKILLKDLLQLTENLN
5855	536	2391	LRSVGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP FISLTHHVLSQSQSPLSSNCWICLSTHTQ*FTALPADLLTWTQS NVSLHISYLAIPFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTQTSFISPPP LCLSRTYPN?AHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY KIISTSAWQKVLCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN

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			FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN ILPPNQTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT GIAGITTSITSYQTLFTTLSNTVEDMHTSITSLQRQLDFLVGVI LQNWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD RAAEL*HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIPISIAGILYK FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL VDYRGYGKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAPAVEPQGPALGSEPMMLGSPTSPKPG VNAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS* NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI DKSVMESSDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMFGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPQDSSKPVVAQGPGPAPGVGSAP PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP PSSGVPTTPPQAGGPPPPPAAVPGPGPGPKQGPGPGGPKGGKMP GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTQRCRFC LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR ALA*NCPKPELG*YTP*GGRQLPSSLFPTHACLPLSCSVIFSPP MFPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCLN FAS
5859	307	1503	GSSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNQSFL RTPIQRTPHEINRRESNRLSAPSYLARSLADVPREYGSSQSFVT EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS VDWTMRGRKYYIDHNTNTTHWSHPLEREGLPPGWERVESSEFGT YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQQTERNQ SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT YQGMLKLLFMKELEQIVKMYEAYRQALLTELENRKQRQQWYAQQ HGKNP
5860	2956	1270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI SWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATI TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP NETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF CYRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSV KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
5861	2051	1305	EVCACVQAFWLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAPAQQPAG/EPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI LE*RMNSGSPARDNAPSQRFCTNLSEGLRFGISPSWREALYGCH

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			A
5862	1556	483	PPFQLIMGEIKVSPDYNWPRGTVPLKKIIVDDDDSKIWSLYDAG PRSIRCPLIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW DHLEFCDGFRKLLDHLQLDKVHLFGASLGGFLAQKFAEYTHKSP RVHSLILCNSFSDTSIFNQTWTANSFWLMPAFMLKKIVLGNFSS GPVDPMMADAIDFMVDRLESLGQSELASRLTLNCQNSYVEPHKI RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPRSLRCRKA ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRPFPSGSSGS PVLTVSGK
5863	2714	249	PFPSRGSLPLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPQN VNISGGTFTLSHGWAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRLGSYPVGGNVSF ECRDGFI\LRGSPVRQCRPNGMWDGETAVCDNGAGHCPNPGISL GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECQGNGVWSGTE PICRQPYSYDFPEDVAPALGTSFSHMLGATNPTQKTKESLGRKI QIQRSGHLNLYLLLDCSQSVSENDFLIFKESASLMVDRIFSFSI NVSVAIITFASEPKVLMSVLNDNSRDMTEVISSLENANYKDHEN GTGTNTYAALNSVYLMMNNQMRLLGMETMAW\QEIRHAIILL\T DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV DWRELNELGSKKDGERHAFILQDTKALHQVFEHMLDVSKLTDTI CGVGNMSANASDQERTPWHVTIKPRSQET\C\RGALISDQWVLT AAHCFRDGNDHSLWRVNVGDPKSQWGKEFLIEKAVISPGFDVFA KKNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \RANLGFLRETFKGSTCR\DHENEL/VWNKQSV\PAHF\VAL\N GSKLEHLTLRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRE\VVT D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LFP Q*SPWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLEFLPS EWATLRTL
5864	173	1013	PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDNDSK*PRNGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPFCSPG/PPPQVPSP/TRSFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSPSSNIKIQPSSWLIWQQP
5865	568	1684	CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWNAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK
5866	98	3197	ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL

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			NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILQNHTEIVFAR TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI AGSDVSKQAADMILLDDNFASIVTGVEEGRLIFDNLKKSIAYTL TSNIPEITPFLLFIMANIPLPLGTITILCIDLGTDMVPAISLAY EAAESDIMKRQPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV YDEIRKLILRRNPGGWVEKETYY
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRPPKAPE DPSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQQNKK ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GQPQPHPPR/IDI WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA PDRCSDDA*QSCPAAAAAAPLQRQCDQSQGQITSPQSGNSGETFS ESWQRGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5870	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5871	3	3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDILDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHRIL QKLNDCSCLASQAILLGILLKREGPNFITKEGTVSDHIERVYRR

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			AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAFG EEEEVISNPLSPRVIQNIIYYKCNTHDERRAVIQQELVIHIGWI ISNNPELFSGTLKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP SEVKQLLLDILQPCQNGRCWLNRRQIDGSLNRTPTGFYDRVWQI LERTPNGIIVAGKHLPQQPTLSDMTMYEMNFSLLVEDTLGNIDQ PQYRQIVVELLMVVSIVLERNPELEFQDKVDLDRLVKEAFNEFQ KDQSRLKEIEKQDDMTSFYNTPPLGKRGTCSYLTKAVMNLLLEG EVKPNNDDPCLIS
5872	68	665	VQGYMYRFVIKINSCYSEKTSICRHRCCPELPATQPWPTPTVFF NIAIDSESLGCI\SFKLFADKV/PKRWKKNFVLLNTCEKVLGDK GPCFYRIIPG\LCQGGDPTHHNGTGGKSLYSKEFDDENFI/LKH TAPGVLSTANAGPTTNGSQFFICTAKTEDG*QHVVFGKVKDGMS IVEALERSGSRNGKTSKKITAANCGQL
5873	2240	506	RRPPEGGSCGGRRTRARMPLPWSLALPLLLSWVAGGFGNAASAR HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF GECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGS YKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCP SSGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCH IGPELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKC KQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMK KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGG\KKG NEEKMKEGLEDEKREEKALKD*HRRERPFRG\DVFFPKVNEAGE FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\ EDDFDW\NPADR\DNAI\GFY\MAVPGLWQGHK\KDIGRLKLLL PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSE DEKWKTGKIQLYQGTDATKSIIFEAERGKGKTGEIAVDGVLLVS GLCPDSLLSVDD
5874	2	3387	ACPRLARRRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDNKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRPGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALETPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLESVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKAEPEPMREEEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GRAEFEDEPPPRRAELESPEVMPEEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGNKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF
5875	296	1848	LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS /SGDPSCPRRGAAPDIWPYPQQRCLHSPNWQHQT\SHGTESSGS

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			GLFALCTLDGTLKLMEEMEEADKLLWSVQVDHQLFALEKLDVTG NGHEEVVACAWDGQTYIIDHNRTVVRFQVDENIRAFCAGLYACK EGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST TACCRSWAWILTTSL*LVPCFTKRSTIQTSHHSVLPQASRIPPS WTCLIAGEGFF*TPTLPPKGVFGSHCAAAGSITKQ
5876	1122	224	HLPLGVPSKVAGAAAMEPQEERETQVAAWLKKIFGDHPIPQYEV NPRTTEILHHLSERNRVRDRDVYLVIEDLKQKASEYESEAKYLQ DLLMESVNFSPANLSSTGSRYLNALVDSAVALETKDTSLASFIP AVNDLTSDLPRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDV KKAELHLSTER\AKVDNRRQNM\DFLKAKSEEFRFGIQAAGEQL SARGQ\DAFSVPIQSLVALIRENWPRLKQQTIPLK\KKLESYLD LMP\NPSHCSK*RIEEAK\RELA\SIEAELTRRVS\MMEL
5877	2030	1907	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV LSRELIEMLAISRNQKLLQAGEENQVLELLIHRDGEFQELMKLA LNQGKIHHEMQVLEKEVEKRDSDIQQLQKQLKEAEQILATAVYQ AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGD PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/RRKIAR CPCSTVS/NGSQMTCR*INILILQKSVCEL
5878	950	2113	GLWKCMQLQGPHTHRVQP*PTPRQQGPQ\VPVAVIAGNRPNYLY RMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTP ISIKNARVSQHYKASLTATFNLFPEAKFAVVLEEDLDIAVDFFS FLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG LGWVLRRSLYKEELRPKWPTPEKLWDWDMWMRMPEQRRGRECII PDVSRSYHPGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL KKEAYEVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTYVAFIR MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV GVPASPYSVKKPPSVTPIFLEPPPKREGAPGAPEQT
5879	3	981	RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL AIAMVRFYMEKGTHRGLYKSIQKTLKFFQTPALLEIVHCLIGIV PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT EITRYSFYTFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCPFQNNQDYLSPSF NNKNKQLCEISWIVWFLKI
5880	1138	1324	SLWCLVAGGLGLGPSSQNPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ
5881	26	441	GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV
5882	2407	2216	SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*IHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEPILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCRRYLFICRFFVVSGPAAHDLFHAVMGRTLSMTLKHLDSY LADCYDAIAVFLCIIHIVLRFRNIAAKRDVPALDRYWEQVLALLW

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			PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV SINQTIPNERTMQLLGQLQVEVKNFVLRVAABFSSRKEQLVFLI NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEPIEELLS PPFGGLVAFVKEAEALIERGQAERLRGEEARVTQLIRGFGSSWK SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRFHRV\L SQPQLRALPARAELINIHHLMVELKKHKPNF
5883	2	1374	EFPGRRFRAVMEAGAGAGAGAAGWSCPGPGPTVTTLGSVEASEG CERKKGQRWGSLERRGMQAMEGEVLLPALYEEEEEEEEEEEVE EEEEQVQKGGSVGSLSVNKHRGLSLTETRLEELRAQVLQLVAEL EETRELAGQHKDDSLELQGLLEDERLASAQQAEVFTKQIQQLQG ELRSLREEISLLEHEKESELKEIEQELHLAQAEIQSLRQAAEDS ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNEKYRALQESNS SLTGQLADLESERTQRATERWLQSQTLSMTSAESQTSEMDFLRP DPEMQLLRQQLRDAEEQMHGMKNKCQKLCCELERLQHHRQVSEE EQRRLQRELKCAQNEVLRFQTSHS\SPSHPLPPIPPSSPCLL*A LVVISALLWCWWAETSS
5884	4261	2522	GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVFVV FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSKACLQF SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVRQM HLLXSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE IPSTSDTKSDTATGGESAGHATSSQEPSGCSDQRPAEDLNIRVE RLTKKJEERREEKRKEEEQREIKKEIERRKTGKEMLDYKRKQEE ELTKRMLEERNREKAEDRAARERIKQQIALDRAERAARFAKTKE EVEAAKAAALLAKQAEMEVKRESYARERSTVARIQFRLPDGSSP TNQFPSDAPLEEARQFAAQTVGNTYGNFSLATMFPRREFTKEDY KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSSGDIW TLLGTVLYPFLAIWRLISNFLFSNPPPTQTSVRVTSSRPPNPAS SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGKDENNTW NGNSTQQM
5885	900	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDEFLDV IYWFRQIIAVVLGVIWGVLPLRGFLGIAGPCLINAGVLYLYFSN YLQIDEEEYGGTWKLTKEGFMTSFA/IVHGHLDHLLHCHPL*LM VYSSQVLPIQSKGPS
5886	86	1341	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFRLKTSELPPLKNG EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAL PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLEETLKKASPDGY DCYFDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLEKPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA
5887	1937	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGPQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPEAN SGNERTILISTAVTFVDVSAPARAGFRAPPAINARLPFNFFFPF V

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5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLP CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL YSTDPKLKDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS FYCETAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDRKS LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\ NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
5889	1831	731	LPAACGRPVTARPRQAPEGRSGRPRDLDPYPPQVFPPRPDRVAI VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL AAEGSHVTANVVDPGVVNTDLYKHVPWATRLAKKLLGWLLFKTP DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH LVRQIP\NTAIMMATYELVVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGPA DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT TPDKLLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY AIPVALQKAGLTVSDVDIFEINE\AFASQAAAYCVEKLRLPP*EG *TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQFQTTVLSVRKCP DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR TAVKNMIEQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLL CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF

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			LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQPLGSIFPT AELQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRIDLFGESQS QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAVRLYFGPCN SY*YRLVGPGQWEGARNAIFTQKQRILKPLKTRALKDSSNFSVS FLLKILGLLAVVVAPF\CQLQWS
5894	174	1673	RYSPKKVLQNKESSLKLGMATALVSAHSLAPLNLKKEGLRVVRE DHYSTWEQGFKLQGNSKGLGQEPLCKQFRQLRYEETTGPREALS RLRELCQQWLQPETHTKEHILELLVLEQFLIILPKRLQARVQEH HPESREDVVVVLEDLQLDLGETGQQVDPDQPKKQKILVEEMAPL KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIVVTDSCGRVES SGKISEPMEAHNEGSNLERHQAKPKEKCIEYKCSEREQRFIQHLD LIEHASTHTGKKLCESDVCQSSSLTGHKKVLS*ERKVIQC\HGV LGKAFQRSSHLVRHQKIHLGEKPYQCNECGKVFSQNAGLLEHLR IHTGEKPYLCIHCGKNFRRSSHLNRHQRIHSQEEPCECKECGKT FSQALLLTHHQRIHSHSKSHQCNECGKAFSLTSDLIRHHRIHTG EKPFKCNICQKAFRLNSHLAQHVRIHNEEKPYQCSECGEAFRQR SGLFQHQRYHHKDKLA
5895	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQIIYIQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAASVAKLLDLKKQLAVAEG KPPEAPKGKKKK
5896	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA

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			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK
5897	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVARG KPPEAPKGKKKK
5898	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEKIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK
5899	326	1078	NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEEIDAKAEEEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLRPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALPGANTNRKFFI
5900	64	1409	KAASRDSPCLEFCPLCGVSSHDLQHRMWYHRLSHLHSRLQDLLK CGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLYGIAFVEN VPPTQEHTEKLAERISLIRETIYGRMWYFTSDFSRGDTAYTKLA LDRHTDTTYFQEPCGIQVFHCLKHEGTGGRTLLVDGFYAAEQVL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QKAPEEFELLSKSAI\KHEYIEDVGRCHQPHDWDWAQS*ISTHG /YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL NTARLLGLQA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL KTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIHFMITSTYYICE SCDKQFTSVDDLQKHLLDMHTFVFFRCTLCQEVFDSKVSIQLHL \AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK CIFCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH DGSEEDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMQTHLGPVKHYM CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFL EHCQMEPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMQKTGN GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVCGL KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID EGLNHECKLCSQTFDSPAKLQCHLIEHSPEGMGGTFKCPVCETV FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ HSS
5902	712	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF IPLXPRQ*ED*MFQSWLHAWGDTLEEAFEQCAMAMFGYMTDTGT VEPLQTVEVETQGDDLQSLLFHFLDEWLYKFSADEFFIP\GWGE EFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVET HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL ATIHGMNRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSP HGGRNCLRC/VHC*HLIFRKDL\GW\KWI\HE\PKGYHANFC\L GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	MMEEIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKFLQQTGG RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEEEKEKKHQKRRQRQFKLKLLLESYTQQKKEQEEFLRLEKEI REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NT=HQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR
5905	287	2912	MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTLFISVYFS*LVFGINGFQYSFVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA* YNLN*I*QF*YKMCHFVLCMSE*SYNICLFIAGF\LWNMDKYTM